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45: gb_htg7:*
46: em_htg1:*
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48: em_htg3:*
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55: gb_htg11:*
57: gb_htg14:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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Query Match

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                                 GAGGCTGTGAGGAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAAC
                                                    GAGGCTGTGAGGAGTGTGTGGAACAGGACCCCGGGACAGAGGAACCATGGCTCCGCAGAAC
                                                                                            CCCCGGTGTGAGGCGGCCTCACAGGGCCGGGTGGGCTGGCCGAGCCGACGCGGCGGCGGAGGCGGAGCCGGCGGGCGGAGCCCGGTGGGCGGGGCGGAGCCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG
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                                                                                                                                                                                                                                               Similarity
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/note="J doma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA88307.1"
/db_xref="GI:6567166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hDj9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Stratagene pancreas"
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ERj3 gene; ERj3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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D-66421 Homburg / Saar, GERMANY
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/note="homolog of yeast
/evidence=experimental
/product="ERj3"
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/db_xref="taxon:9606"
/tissue_type="placenta"
21. .86
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87. .1094
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GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMD
ITHLDGHKVHISRDKITRPGAKLMKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEE
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YRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQYDTYGEEGLKDGHQSSH
GDIFSHFFGDFGFMFGGTPRQDRNIFRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVA
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/protein_id="CAB65118.1"
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/function="putative role in cellular
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                                                         AACAATATCAAGGGCTCTTTGATAATCACTTTTTGATGTGGATTTTTCCAAAAGAACAGTTA 1188
                                                                                         GCTTTGAGATGGATATTACTCACTTGGATGGTCACAAGGTACATATTTCCCCGGGATAAAG
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Patent: WO 9928461-A 10-JUN-1999;
LEADD B V (NL); DANEN VAN OORSCHOT ASTRID
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Danen-Van,O.A. and Noteborn,M.H.
METHODS AND MEANS FOR INDUCING F
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1. .745
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/db_xref="taxon:32644"
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Pred. No. 3.6e-131;
0; Mismatches 74;
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                           583 AGAGGAAGTGATATTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAAT
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                                                                                                                    GAGGAATGCCTCAAGAAGGAGGGCATGATGGATCACGGTGGTGATCCGTTCTCTAGCTTC
                                                                                                                                       GAAGAAGGATT---AAAAGATGGTCATCAGAGCTCCCCATGGAGACATTTTTTCACACTTC
CGAGGCGCCGATATCGTAATGGACTTGTACGTTTCCCTGGAGGAGCTATACTCCGGAAAC
                                                                              CAGCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCCCAGGAGAAATTCCAGGATCTG 405
                                                                                                                                                                                                                                                                                                    AACGTAAAGAAAAACGCCAACACGAACGAAGTGAAGAAGGCGTATCGCCGTTTGGCCAAG
                                                                                                                                                                                                                                                                                                                        GGGGTGCCTCGAAGTGCCTCTATAAAAGGGATATTAAAAAGGCCTATAGGAAACTAGCCCTG 345
                                                                                                                                                                                                                                                                                                                                                               GGAGCGGCCTACGAAGTCCTCTCCAATCCGGACAAACGGAAGACCTACGACCGCTGCGGC
                                                         TTTGGGGACTTCGGCTTTCACTTCGGTGGTGATGGCCAGCAGCAAG-----ATGCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was identified as CDM:10209998 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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AC017242
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-DEC-1999) Celera Genomics,
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Pred. No. 3.7e-65;
0; Mismatches 392
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                                                                                                                                                                        Pterryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 104278)
Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pefeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.
Sequencing of Drosophila chromosome, region 21C3-21C7
unpublished (1997)
2 (bases 1 to 104278)
2 (bases 1 to 104278)
Celniker,S.E., George,R.A., Galle,R.F., Hoskins,R.A.,
Celniker,S.E., George,R.A., Agbayani,A., Arcaina,T.T., Baxter,E.,
Svirskas,R.R., Harris,N.L., Agbayani,A., Arcaina,T.T., Baxter,E.,
Blazedj,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E.,
Elanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Flanagan,J., Houston,K.A., Hommasti,S.R., Karra,K., Kearney,L.,
Kim,S.H., Lee,B., Lomotan,M.A., Mak,J., Mazda,P., Mok,M.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and relationship to other sequences, please visit our sequence/) archive Web site (http://fruitfly.berkeley.edu/sequence/) email to drosophila@mhgc.lbl.gov.
Library locations: 135-8, 21-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For further information about this sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawrence Berkeley National Berkeley, CA 94720
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CE 1 (bases 1 to 145017)

RS Muzny, D.M., Adams, C., Balley, M., Barbaria, J., Blankenburg, K., Burket, C., Burcows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Durbin, K.J., Fernandez, C., Ferraguto, D., Jakyon, D., Dugan-Rashid, N., Correll, J. H., Gorrell, L. L., Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Lucler, R., Martin, R., Martinez, G., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Shah, E., Shah, E., Shah, B., Paxton, S., Payton, B., Perez, L., Pu, L. L., Garler, S., Shah, E., Shah, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Watliamson, A., Walliamson, A., Warliamson, A., Wa
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                                                                                                          Direct Submission
Submitted (09-DEC-1999) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                    Baylor Plaza, Houston, TX 77030, USA
On Feb 19, 2000 this sequence version replaced g1:6671836
                                                                                                                                                                                                                                                                             Worley, K.C.
                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                   Department
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* arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence 
* as soon as it is available and the accession number will 
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.980611
Consensus quality: 90208 bases at least Q40
Consensus quality: 108595 bases at least Q20
Consensus quality: 118331 bases at least Q20
Estimated insert size: 145017; agarose-fp estimation Estimated insert size: 13603; sum-of-contigs estimation
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Center clone name: RP11-35G16
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3383: contig of 847 bp in length
3403: gap of unknown length
4441: contig of 1038 bp in length
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4: contig of length
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Best Local Similarity 98.9%;
Matches 265; Conservative
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Worley.K.C.

Direct Submission
Submitted (09-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Feb 19, 2000 this sequence version replaced gi:6671836.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145017)
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//db_xref="taxon:9606"
/clone="Rell-35G16"
a 30419 c 31541 g 41252 t
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NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Chemistry: Dye-terminator B1g Dye: 100% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 90208 bases at least Q40
Consensus quality: 108595 bases at least Q30
Consensus quality: 118331 bases at least Q30
Consensus quality: 118331 bases at least Q30
Estimated insert size: 145017; agarose-fp estimation
Quality coverage: 1.4x in Q20 bases; agarose-fp estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.
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                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-SEP-1995) Genethon, B.P. E-mail: Jean.Weissenbach@genethon.fr 2, (bases 1 to 332)
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1 (bases 1 to 332)
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                                                                         8.2%;
95.0%;
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                                                                         Score 113; DB 13; Pred. No. 2.8e-16;
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                                                                                                                                                            TTCCACACGAGTGCCCCTTTGGCCAAAGAAGATTATTATCAGATATTAGGAGTGCCTCGA 337
GACACAAATAAGGATGATCCCAAAGCCAAGGAGAAGTTCTCCCAGCTGGCAGAAGCCTAT
                                       GACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTTAT 417
                                                                              AATGCCAGCCAGAAAGAGATCAAGAAAGCCTATTATCAGCTTGCCAAGAAGTATCACCCT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-APR-1998) Pathology, Harvard Medical School, 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A novel human DnaJ protein, hrid-1, a homolog of the Drosophila tumor suppressor protein fid56, can interact with the human papillomavirus type 16 E7 oncoprotein fid56, can interact with the human papillomavirus type 16 E7 oncoprotein virology 247 (1), 74-85 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schilling, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2656)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98354343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tumorous imaginal discs protein Tid56 homolog"
/protein_id="AAC29066.1"
/protein_id="AAC29066.1"
/db_xref="GI:337677"
/transilation="MAARCSTRWLLVVVGTPRLPAISGRGARPPREGVVGAWLSRKLS
VPAFASSLTSCGPRALLTLRCGVSLTCTKHNDFICTASFHTSAPLAKEDYYQLIGVPR
NASQKEIKKAYYQLAKKYHPDTNKDDPKAKEKFSQLAEAYEVLSDEVKRQYDAYGSA
GFDGAGSGGHSYWKGGPTVDPEELFRKIFGEFSSSSFGDFOTVFDQPGEYMELTEN
QAAKGVNKEFTVNIMDTCERCNGKGNEPGTKVQHCHYCGGSGMETINTGPFVMRSTCR
                                                                                                                                                                                                                                                                                                                                                                            MDSSAGSKARREAGEDEEGFLSKLKKMFTS"
                                                                                                                                                                                                                                                                                                                                                                                              RCGGRGSIIISPCVVCRGAGQAKQKKRVMIPVPAGVEDGQTVRMPVGKREIFITFRVQ
KSPVFRRDGADIHSDLFISIAQALLGGTARAQGLYETINVTIPPGTQTDQKIRMGGKG
IPRINSYGYGDHYIHIKIRVPKRLTSRQQSLILSYAEDETDVEGTVNGVTLTSSGGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hTid-1 protein; DnaJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="TID1"
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                                                                                                                                                                                                                                    Score 101.4; DB 11;
Pred. No. 1.6e-13;
0; Mismatches 101;
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                   CCACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTGTTATGAGGTTCTGTCAGATAGT 435
                                                                            ATTAAAAAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGAT 375
                                                                                                                                         ATTGCCGGACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGAT 315
CCAGCTGCAGTAGAGAATTTAAAGAACTTACAGTTGCATATGAAGTTTTATCTGATACT
                                                                                                                      ATGCCCGATAATAAATTTTATGATATTTTAGGAGTTGCACGTGATGCATCAGAAACTGAT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rauchenberger,R., Schwartz,J.M. and Maniak,M.
Cloning and analysis of a DnaJ homologue reveals its dual
localisation in the cytoplasm and cortex of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-MAY-1998) Zellbiologie, Klopferspitz 18a, Martinsried 82152,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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nilarity 62.4%;
Conservative
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KEKELTVAYEVLSDTEKRELLDKYGEEGLKEGGAGGFSGDDIFSLFFGGGGFGGFGGRG
GRRGPRKGEPLQHNLKVTLEDLYKGKVQKLALQKSSKCPDCAGKGSTSKDGVKKCDDC
HGQGFKYIHOJGPGMYQKLQSQCPSCKGEGNVIREKORCPKCKGNKTIQEKKTLEVN
IDKGMKHGQKIVFPEEGDYESPDIVPGDVIVVLVQKEHPVFQRDGDDLVMEHELTLLE
ALTGFTFYITHLDGRVITVKNPPTQIIKQGDIKCIYNEGMPGYKRPEEKGRLFIKFNV
VFPTSGQITPENAKLLEKILPKPKPVQKPVSHDGIDEEAVLHDFDTKQHSHSRSSAYD
DDDEDQHGGHPQGVSCAQQ"
363 t
                                                                                                                                                                                                                                                                                                                                                                                                                /product="heat shock protein Ddj1"
/protein_id="AAC72887.1"
/db_xref="GI:3859851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Ddjl"
/note="DnaJ homologue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Dictyostelium/strain="AX3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=]
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                AAACAGTACGATACTTATGGTGAAGAAGGATTAAAAGATGG
                                                          GAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGG
                                                                                         CAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGG
                                                                                                                                                     TATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTG---ATGATCCACAAGCC 384
                                                                                                                                                                                    GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAGGCA 121
                                                                                                                        TATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAAGAAGAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-JUL-1998) Endocrinology, Cedars-Sinai Medical Center, 8700 Beverly Blvd, Los Angeles, CA 90048, USA Location/Qualifiers
1. .975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pituitary tumor-transforming gene protein associates with ribosomal protein 510 and a novel human homologue of bnaJ in testicular cells J. Biol. Chem. 274 (5), 3151-3158 (1999) 99115663
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FTSFGSLGHGGLTSFSSTSFGGSGMGNFKSISTSTKWLMAEKSLQRELSRTVKKE"
180 c 233 g 260 t
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/product="nnaJ-like 2 protein"
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/db_xref="taxon:9606"
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l. .975
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                                                                                                                                                                                                                                                                                                  GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAAGGCA 166
                                                                                                                      GACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTGG
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AB014888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1485)
Saito,T. and Seki,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new member of human dnaj-related gene family Published Only in DataBase (1998) In press
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KFKQYAEAYEVISDAKKRDIYDKYGKEGLINGGGGGGSHFDSPFEEGFTFRNIPDIVFRE
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101. .826
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101. .826
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                             for DnaJ homolog,
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Fax:81-43-251-9818)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-JUN-1998) to the DDBJ/EMBL/GenBank databases. Ry. Hanai, Rikkyo (St.Paul's) University, Department of Chemistry; Nishi-Ikebukuro 3-34-1, Toshima, Tokyo 171-8501, Japan (E-mail:hanai@rikkyo.ac.jp, Tel:81-3-3985-2377)

Location/Qualifiers
1. .1487
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Zhang, W., Wan, T., Yuan, Z. and HSJ2, a novel human homologue
                                            Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
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EEDGQLKSLTINGKEQLLRLDMK"
a 270 c 343 g 438 t
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148. .873
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Pred. No. 3.3e-11;
0; Mismatches 71;
                                                                                                                                                      mRNA
J2 protein
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(HSJ2) ml
 bacterial heat-shock protein
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TITLE
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                                                                                             JOURNAL
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Best Local Similarity 66.5%;
Matches 147; Conservative
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                                                                                                    Eukaryota; Metazoa; Chordata; Vertebrata; Mam
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1557)
Zhang, J.S., Nelson, M., Wang, L. and Smith, D.I.
Direct Submission
                                                    Submitted (21-APR-1998) Pathology and Lab. Medicine, Mayo Clinic, 200 SW 1st St., Rochester, MN 55905, USA Location/Qualifiers
                                                                                                                                                                                                                                                                               Homo sapiens
AF060703
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                               AF060703.1
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                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                    AF060703
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Zhang, W., Wan, T., Yuan, Z. and Cao, X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="heat shock J2 protein"
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Pred. No. 3.3e-11;
0; Mismatches 71; Indels 3;
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                       445 AAACAGTACGATACTTATGGTGAAGAAGGATTAAAAGATGG 485
332 GACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTGG
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FTSFGSLGHGGLTSFSSTSFGGSGMGNFKSISTSTKMVNGRKITTKRIVENGQERVEV
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a 275 c 357 g 452 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="111"
/cell_type="pancreatic cancer cells"
/map="119"
146. .871
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Pred. No. 3.3e-11;
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Search completed: June 30, Job time: 10107 sec 2000, 12:46:48

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Listing first 45
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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AUTHORS
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            Unpublished (1999)
On Mar 10, 1998 this sequence
Contact: Ottenwaelder B
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 681)
Ottonwaelder, B., Obermaier, B., Mewes, H.W., Gassenhub
                                                                                            AL038833 681 bp mRNA EST 27-SEP-1999 DKFZp56600946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp56600946 5', mRNA sequence.
                                      Wiemann,S.
                                                            Homo sapiens
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A122332
N9523973
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AL13388 yf65b01.r
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AL021086 ub01al1.s
AL13375 EST108135 R
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AL04833 vd55a11.s
AL474833 vd55a11.s
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                                         AAGACCCTTTTGAGGACTTCTTTGGGAATCGAAGGGGTCCCCGAGGAAGCAGAAGCCGAG
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1 sequence also available.

2 sequence also available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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/clone_lib="566 (synonym: h
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/note="Vector: pAMP1; Site_
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/db_xref="taxon:9606"
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TGTCGGATGCTAAGAAACGGGACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTG
                                                 CTGAGAATAAAGAAGCAGAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGC 322
                                                                                                             CCGAGGATATTAAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATC
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DKFZP566B1446_r1 566 (s
DKFZP566B1446 5', mRNA
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This clone is available at the RZPD
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Clone from S. Wiemann, Molecular Genmee Analysis, German Cancer
Research Center (DRT2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST (Ottenwaelder, et al.)
Unpublished (1999)
On Reb 18, 1999 this sequence version
Contact: Ottenwaelder B
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/db_xref="taxon:9666"
/clone=NbKT2p566B1446"
/clone_lib="566 (synonym: h
/tissue_type="kidney"
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                                                                                                                                                                                                                                                                                            This clone is available royalty-free th
IMAGE Consortium (info@image.lln1.gov)
Insert Length: 1524 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 8, 1995 this sequence Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996) 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasee,S., Dietrich, M., DuBque,T., Favello,A., Gish,W., Hawkins,M., Hutman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R., and Marra,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA020916 646 bp mRNA EST ze64h08.rl Soares retina N2b4HR Homo sapiens mAGE:363807 5' similar to PIR:S23509 S23509
                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 44444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata;
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                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                      quality sequence stop: 428.
Location/Qualifiers
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                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:1280510"
/db_xref="taxon:9606"
/clone="IMAGE:363807"
/clone_lib="Soares retina N
/tissue_type="retina"
/dev_stage="55 year old"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                         /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  version replaced
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v) for further
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                                                                                                                                                                   TTTTGATACAGGATT 638
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                                                                                                                                                                                                                                                                                                                                                                                              CGGATGCTAAGAAACGGGACATCTATGACAAATATGGCAAAGAAGAAGATTAAATGGTGGNG
                                                                                                                                                     CTTTGATACAGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCG
                                                        AA496105 553 bp mkNA
zv5lb10.r1 Soares_testis_NHT
5' similar to SW:HSJI_HUMAN F
                             AA496105.1
                                         mRNA sequence.
AA496105
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Pred. No. 1.4e-12
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                                                               P25686
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l.4e-126;
                                                             sapiens cDNA clone
6 DNAJ PROTEIN HOMOI
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                           GGCTTCACATTCCGTAACCCAGATGATGTCTTCAGGGAATTTTTTTGGTGGAAGGGACCCA
                                                                                                                                              GTCCTCGGACCCATTCCAACAATCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGGC 119
                                                                                                                   GCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGGGACATCTATGACAAATATGGC 363
                                                                                                                                                                                                                                                                                                                          GCTGTGAGGAGATTCGGGCCGTCACCCTGCCTCCCCTGCGTCCCG-CACCGGCCGCTTCT 59
                                                                                                                                                                                                                                                                                                                                                                                         547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 553)
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Yector: p77T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
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/clone="IMAGE:757147"
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/db_xref="GDB:5977757"
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Pred. No. 1.2e-125;
0; Mismatches 6;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information insert Length: 700 Std Error: 0.00
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h quality sequence stop: 457.
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                           Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 143 c 89 g 152 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:1624722"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              38.1%;
97.7%;
                                                                                                                               Score 506.6; DB 40;
Pred. No. 3.4e-121;
0; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1798756
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                         High quality sequence stop: 450.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov cDNA Library Preparation: M. Bento Soares,
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                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1649657"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
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. Fatima Project (CGAP),

Sequencing Center information can be

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RESULT
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IMAGE:2236276 5' similar t
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AW106720.1 GI:6077520
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                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                            AW106720
                                        house mouse.
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/note="Organ: parathyroid gland; Vector: pT7T3D
/note="Organ: with a modified polylinker; Site_1: Not
Site_2: Eco RI; 1st strand cDNA was primed with a No
oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
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97.9%;
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Pred. No. 1.2e-118;
                                                                                                   kidney mkia Mus musculus cDNA clone r to TR:054946 O54946 MRJ. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                     123 TTTCCTCGGACCCATTCCAACAATCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGG 182
                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                 CAAAGAAGGATTAAA---TGGTGGNGGNGGNGGTGGAAGTCATTTTGACAGTCCATTTGA 419
                                                                                              AGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGGGACATCTATGACAAATATGG
                                                                                                                                                                                CAAAGAAGGATTAAATGGTGGTGGAGGAGGAGGTGGAATTCATTTTGACAGTCCATTTGA
                                                                             AGCTGAGGCATATGAAGTGTTATCGGATGCTAAAAAGCGGGACATCTACGACAAATATGG
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                                                                                                                                                                                                                                                                            CGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAGGCATATCGGAAACTGGCACTGAA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free t. IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
On Jul 7, 1999 this sequence version replaced Other_ESTs: um32g03.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 675)
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 438
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //note-Porgan: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACGTGTGF); Site_2: DraIII (CACGATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TCTTGGCTACTGG] digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACGATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTCGACCTCGACCACACACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2236276"
/clone_lib="Sugano mouse
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
on May 9, 1995 this sequence version replaced
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W63690 661 bp mRNA EST 11-OCT-1996 zc58all.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326492 5' similar to PIR:S23509 S23509 dnaJ protein homolog human; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 661)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Insert Length: 1745 Std Error: 0.00
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The WashU-Merck EST Project
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Eutheria; Primates;
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EST.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                      primer: ETPrimer
                                                                                                                                                                                                                                                                quality sequence stop: 407
Location/Qualifiers
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Site_2: Eco RI; 1st strand cDNA was primed with oligo(dT) primer
                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:326492"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:1260694"
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                                            T-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
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     8 others
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RESULT
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559; Conser
AL036026 531 bp mRNA ES;
DKFZp564P0422_r1 564 (synonym: hfbr2) Homo
DKFZp564P0422 5', mRNA sequence.
AL036026
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2.5e-116;
nes 31;
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KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION DEFINITION

AL036026.1 numan

GI:5405652

sapiens

REFERENCE

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
1 (bases 1 to 531)

and Wiemann

AUTHORS

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                                                                CATTTTCATTTGACTTCTTTGAAGACCCTTTTTGAGGACTTCTTTTGGGAA 530
                                                                                             GCAAAGAAGGATTAAATGGTGGNGGNGGNGGTGGAAGTCATTTTGACAGTCCATTTGAAT
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                                                                                                                                        GCAAAGAAGGATTAAATGGTGGAGGAGGAGGTGGAAGTCATTTTGACAGTCCATTTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Unpublished (1999)
On Jun 22, 1998 this sequence version replaced
Contact: Wambutt R
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo saplens"
/db_xref="taxon:9606"
/clone="DKFZp564P0422"
/clone_lib="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="x1-2blue"
/note="vector: pAMP1; Site_1: Not1;
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Query Match
Best Local :
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                                                                    GNGGNGGNGGTGGAAGTCATTTTGACAGTCCATTTGAATTTTGGCTTCACATTCCGTAACC
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Unpublished (1999)
On Mar 16, 1998 this sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="bkr2p566:12347"
/clone=lib="566 (synonym: h
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="%1-2blue"
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Pred. No. 4.4e-114;
0; Mismatches 16;
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ATGCCTCACCCGAGGATATTAAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAG 253
                                                                                     CCATTCCAACAATCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGGCCGTGCAGAGAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTCGGGCCGTCACCCTGCCTCCCCTGCGTCCCGCCACCGGCCGCTTCTGTCCTCGGAC 60
                                                                     CCATTCCAACAATCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGAC
                                                                                                                                                                                                             502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40RP from Gibco
High quality sequence stop: 373
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Pran
I.M.A.G.E. Consortium DNA Sequencing by: Washington Uni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 18, 1998 this sequence version Other_ESTs: xb32g09.x1
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa;
Eutheria; Primates;
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                                                                                                                                                                                                                           Similarity
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                           /note="Organ: lung, cell line; Vector: pCMV-SPORT6; Site_1: ECORV; Site_2: NotI; Cloned unidirectionally, 5' adaptor. Primer: Oligo dT. Full-length library constructed by Life Technologies."

117 c 141 g 131 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2578048"
/clone_lib="NCI_CGAP_Lu31"
                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="fetal, 14 wk post-conception"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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Pred. No. 6.3e-113;
0; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU080965
5', mRNA
                                                                                                                                                                                                                                                                                 Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
On Jun 5, 1998 this sequence version replaced
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
                                                                                                                                                                                                                                                                                                                                                                                                                 Hashimoto, K., Kusuda, J., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S. Isolation of full-length cDNA clones library made by oligo-capping method
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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          Sugano mouse brain
                                                                                                                                                                                              /clone_lib="Sugano mouse
/sex="female"
                                                                                                                                                                                                                                     /strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                   /lab_host="TOP10"
                                                                                                                                                                              /dev_stage="adult"
                                                                                                                                                                                                                         /clone="MNCb-6291"
                                                                                                                                                                                                                                                                /organism="Mus musculus"
 161 c
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205 g
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Homo sapiens
Eukaryota; Metazoa; (
Eutheria; Primates; (
1 (bases 1 to 535)
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DKFZp564J1863_r1 564 (synonym: hfbr2)
DKFZp564J1863 5', mRNA sequence.
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14; Conservative
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         Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
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Pred. No. 9.5e-113;
0; Mismatches 145;
                                                                                       Homo
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This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, He
Berlin-Charlottenburg, GERMANY; Email: clone@r
Location/Qualifiers
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
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Clone
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/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
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WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should i
kept in mind should you use this clone.
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This clone is available royalty-
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On Jan 14, 1998 this sequence version repl
Contact: Marra MyMouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
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The WashU-HHMI Mouse
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Eutheria; Rodentia;
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/clone_lib="Sugano mouse
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NISM NCE ORS E	RESULT 1 AW131601 735 bp mRNA EST 27-OCT-1999 LOCUS AW131601 735 bp mRNA EST 27-OCT-1999 DEFINITION xf32a01.x1 NCI_CGAP_Brn50 HOMO sapiens cDNA clone IMAGE:2619720 3' similar to WP:T15H9.1 CE01664 HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR; mRNA sequence. ACCESSION AW131601.1 GI:6133208 KEYMORDS EST. SOURCE human.	312.6 22.7 417 48 A16.14268 312 22.7 451 24 M42272 311.6 22.6 658 63 A1980687 307 22.3 497 74 AW199669 305.6 22.2 449 22 R72989 305.2 2.1 370 36 AA607886 304 22.1 370 36 AA607886 304 22.1 370 36 AA607886 304 22.1 370 36 AA607886 300.4 21.8 413 25 N86926 300.4 21.8 413 25 N86926 300.4 21.8 411 45 A1351856 300 21.8 311 45 A1351856	24 387.2 28.1 426 31 AA280838 25 375.4 27.3 683 51 AI742784 26 369.2 26.8 37. 63 AI772784 27 35.2 25.6 455 26 W56612 28 344.4 25.0 399 48 C84272 29 341.4 24.8 382 80 AW376471 30 339.4 24.7 351 43 AI702493 31 339 24.6 453 34 AA497706 32 33.4 24.4 378 74 AW207301 33 330.4 24.0 346 36 AW343228 34 315.8 23.0 631 80 AW343228	10 445.2 32.4 556 80 11 441 32.0 531 35 12 439.8 32.0 750 41 13 423.8 30.8 438 26 14 417 30.3 726 60 15 415.4 30.2 480 69 16 406.6 29.5 487 34 17 400 29.1 449 26 18 399 29.0 498 30 19 397.6 28.9 501 37 20 394.8 28.7 721 62 23 387.6 28.2 423 26 23 387.2 28.1 394 36	Score Match Length DB ID 681 49.5 735 69 AW131601 627.2 45.6 656 64 AW027159 619.4 45.0 695 36 AA639658 572.8 41.6 655 40 AA984302 484.8 35.2 498 36 AA599885 481.2 35.0 488 35 AA581995 481.2 35.0 488 35 AA581995 486.8 34.7 482 25 N93316 455.6 33.1 791 61 AI819362 445.4 32.4 767 39 AA817574
Qy 883 CCTCACGTGGATGGGACCTGGAGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCA	763 763 241 301	Qy 523 Db 1 Qy 583 Db 61 Qy 643 Db 121	Not I - oligo(dT) primer Double-stranded cito Eco RI adaptors (Pharmacia), digested will cloned into the Not I and Eco RI sites of the PMT73 vector. This library is normalized. I constructed by Bento Soares and M. Fatima Be BASE COUNT 228 a 132 c 203 g 168 t 4 others ORIGIN Query Match 49.5%; Score 681; DB 69; Length 735; Best Local Similarity 96.9%; Pred. No. 1.1e-157;	Possible Seq prime Seq prime High qua. FEATURES source	Tel: (301) 496-15 Email: Robert_Str Tissue Procuremen CDNA Library Pre CDNA Library Arr DNA Sequencing b Clone distributi found through the www-bio.llnl.gov/

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/lab_host="Medulloblastoma"
/lab_host="Medulloblastoma"
/note="Organ: brain; Vector: pTT3D-Pac (Pharmacia) with a modified polyllnker; 1st strand cDNA was prepared from medulloblastoma tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT773 vector. This library is normalized. Library constructed by Bento Soares and M. Fatima Bonaldo. "
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sation/Qualifiers
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ry Preparation: M. Bento Soares, Ph.D.
ry Arrayed by: Greg Lennon, Ph.D.
ring by: Washington University Genome Sequencing Center-
ribution: WCI-CGAP clone distribution information can be
ph the I.M.A.G.E. Consortium/LLNL at:
l.gov/bbrp/image/image.html
ATGGATATTACTCACTTGGATGGTCACAAGGTACATATTTCCCGG
                                                          GGAGATGATTTGTACACAAATGTGACAGTCTCATTAGTTGAGTCA
                                                                                 GGAGATGATTTGTACACAAATGTGACAGTCTCATTAGTTGAGTCA 1002
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Pred. No. 1.1e-157;
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Matches 643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40Up from Gibco
High quality sequence stop: 452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Jun 5, 1998 this sequence version replaced gi:3189254. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wt72b07.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2512981 3' similar to wp:T15H9.1 CE01664 HYPOTHETICAL 39.9 PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR; mRNA sequence. aw027159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                              Similarity
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theria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 656)
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185 c 114 g 205 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                              45.6%;
98.0%;
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                                                              Score 627.2;
Pred. No. 2e-1
0; Mismatches
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similar to
            cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                  Unpublished (1997)
On May 9, 1995 this sequence
Contact: Robert Strausberg, P
Tel: (301) 496-1550
                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D.,
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National Cancer Institute, Cancer Genome Anatomy
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//www-bio.llnl.gov/bbrp/image/image.html
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NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1158972
WP:T15H9.1 CE01664 DNAJ ;, mRNA sequence.
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Seq primer: -40ml3 fwd. ET from

High quality sequence stop:

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GCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
                                                                                                                    TTTTGATGTGGATTTTCCAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACA 1217
                                                                                                                                                                         GAAAGGGGAAGGGCTCCCCCAACTTTGACAACAACAACAATATCAAGGGCTCTTTGATAATCAC 1157
                                                                                                                                                                                                                                                             AATAAAATTGGACTTTGTTTAAAATAAGTGAATAA 1312
                                                                                                      TTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACA
                                                                                                                                                         GAAAGGGGAAGGGCTCCCCAACTTTGACAACAATATCAAGGGCTCTTTGATAATCAC
                                                                                                                                                                                                          TGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAA 219
                                                                                                                                                                                                                           TGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAANTANTGGAA 1097
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                                                                                                                                                                                                                                                                                                                 CCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGAGGAGATGATTTGTACACAAA 339
                                                                                                                                                                                                                                                                                                                             CCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAA 977
                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGGA
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188 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .695
/organism="Homo sapiens"
/oref="taxon:9606"
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/clone="IMAGE:1158972"
/clone_lib="NCI_CGAP_CO9"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with
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96.8%;
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Pred. No. 1.7e-142;
0; Mismatches 18;
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AA984302/c
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Best Local Similarity
Matches 622; Conser
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JOURNAL
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashUNCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Sep 12, 1996 the Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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am83g01.s1 Stratagene schizo brain S11
IMAGE:1629744 3' similar to WP:T15H9.1
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: Bluescript SK.; Site_1: EcoRI; Library constructed from S-11 frontal lobe, male, 34 years old, 50% caucasian, 50% Aleutian. Schizophrenic suicide. Random primed into EcoRI site of ZAP II Vector. Mass excised. Custom library. Avg insert length 1.4kb. Material obtained by Johnston N., Torrey, E.F., Yolken R., and the Stanley Neuropathology Consortium - Analysis of RNAs from the Brains of Individuals with Psychiatric Diseases (Unpublished) Stanley Neurovirology Laboratory, Johns Hopkins School of Medicine, Baltimore MD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamyoin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1629744"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Stratagene schizo brain
/sex="male"
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95.1%;
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                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                       Score 572.8;
Pred. No. 5.2
                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1376 Std Error: 0.00
                                                                                                                                                                                                                                     On May 9, 1995 this sequence version replaced contact: Wilson RK / Jia L WashU-MBANHGRI EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA599885 498 bp mRt
ag32ell.sl Jia bone marrow
IMAGE:1091276 3' similar to
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1 (bases 1 to 498)
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quality sequence stop: 359.
   Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1091276"
/clone_lib="Jia bone mar:
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 bone marrow stroma"
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EST.
                                                                                                                                                                                              AA581995 488 bp mRNA EST 05-SEP-1997 nn36d05.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1085961 similar to WP:T15H9.1 CE01664 DNAJ ;, mRNA sequence. AA581995
National Cancer Institute, of Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Verte
Eutheria; Primates; Catarrhini; Hominidae; Hc
1 (bases 1 to 488)
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap;
                                                                                                                                        Homo sapiens
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/tissue_type="bone marrow stro
/dev_stagey="mixed"
/lab_host="XL1-Blue MRF'/SOLR"
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Pred. No. 2.5e-109;
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop:
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/db_xref="taxon:9606"
/clone="IMAGE:1085961"
/clone_lib="NCI_CGAP_GC5"
/tissue_type="germ cell tumor"
/lab_host="SOLR (kanamycin resistant)"
/lab_hos
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                                                                                                                                      817 CTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGGAGTACCCCCTTTATTGGAGAA 876
                                                                                                                                                                                                   Local Similarity
                                                                            GGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCCGAATCAAAGTTGTCAAG 936
                                                                                                                     CTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGGAGTACCCCTTTATTGGAGAA 423
                                                           GGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCCGAATCAAAGTTGTCAAG 363
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1 (bases 1 to 482)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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IMAGE:308860 3' similar to WP:T15H9.1 CE01664 DNAJ ;, mRNA
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                                                                                                                                                                                                                                                                      quality sequence stop:
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/clone_lib="Soares_fetal_lung_NbHL19W"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:1252273"
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                                                                                                                                                                                                 34.7%;
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                                                                                                                                                                                              Score 476.8; DB 25; Pred. No. 2.3e-107;
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by Bento

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                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -400r 110m -2-1 469. High quality sequence stop: 469. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
On Jun 5, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 791)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40Up from Gibco High quality segmence the
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHFP pool 1: 309384-330919, 323208-325895 Soares NbHPP pool 1: 150407, 151176-152327 Soares NbHFR-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2369565"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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                                                                 Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                 AA837554 767 bp mRNA EST 0e31e05.51 NCI_CGAP_Pr25 Homo sapiens cDNA clone similar to WP:T15H9.1 CE01664 DNAJ ;contains alu element; mRNA sequence.
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 767)
                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat
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                                        Tissue Procurement:
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cDNA Library Preparation: Stratagene, cDNA Library Arrayed by: Greg Lennon,
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                                                   Robert_Strausberg@nih.gov
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Soares and M. Fatima Bonaldo."
186 c 114 g 254 t 3 others
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95.0%;
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Pred. No. 4.5e-102;
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AW323622 EST mRNA EST UO74e06.y1 NCI_CGAP_Mam1 Mus musculus cDNA clone similar to WP:T15H9.1 CE01664 HYPOTHETICAL 39.9 K IN CHROMOSOME II PRECURSOR; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Location/Qualifiers
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/clone="IMAGE:1410176"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 445.4; DB 39;
Pred. No. 1.5e-99;
0; Mismatches 18;
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             AACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGGAGTACCCCTTTATTGG
                                                                              AACACTAGAAGTGGAAATAGAGCCTGTGGTGCTAGATGGCATGGAGTACCCCCTTTATTGG
                                                                                                                                              ACGGAAGTGCAATTGTCGGCAAGAGATGCGGACCACCCAGCTGGGCCCTTGGGCGCGTTCCA 752
                                                                                                                                                                                                          GAATATTCCAAGAGGAAGTGATATCATCGTAGATCTAGAAGTCACTCTGGAAGAAGTGTA 120
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                                                             ACGGAAATGCAACTGTCGGCAAGAGATGAGAACCACACAGCTGGGACCGGGACGCTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Jun 22, 1998 this s
Other_ESTs: u074e06.x1
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National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Rodentia;
l (bases 1 to 556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (301) 496-1550
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quality sequence stop: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_2: NotI; Cloned unidirectionally. Prim Library constructed by Life Technologies. I providing samples: Gilbert Smith, NIH" a 110 c 161 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2648290"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
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On Sep 12, 1996 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 531)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., More, B., Thotelag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA596749 531 bp mRNA EST 19-SEP-19 vm59e09.rl Stratagene mouse Tcell 937311 Mus musculus cDNA or IMAGE:1002568 5' similar to WP:T15H9.1 CE01664 DNAJ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
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h quality sequence stop: 445.
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314 286 1810
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                                                                                                                                                          /dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
/note="Organ: bluescript SK-; Site_1: bluescript SK-; Site_1:
/note="Organ: bluescript SK-; Site_1: bluescript SK-; 
                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1002568"
/clone_lib="Stratagene mouse Tcell
/tissue_type="Tcell"
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                         32.0%;
89.3%;
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Score 441; DB 35;
Pred. No. 1.6e-98;
0; Mismatches 57;
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AI057091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                                                                                                                                Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 445.
Location/Qualifiers
                                                                                                                                                                                                                                                               Unpublished (1997)
On May 18, 1995 this sequence version replaced Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
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                   /db_xref="taxon:9606"
/clone="IMAGE:1676202"
/clone_ilb="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                organism="Homo sapiens"
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gi:811070

contact the

Project (CGAP),

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KEYWORDS
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammal Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 438)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                        sequence.
W65314
   Unpublished (1995)
On Apr 14, 1993 th
                                                                                                                                                                                                                                              W65314 438 bp mRNA EST 1
zd33e05.r1 Soares_fetal_heart_NbHH19W Homo sapiens
IMAGE:342464 5' similar to WP:T15H9.1 CE01664 DNAJ
                            The WashU-Merck EST Project
                                             Wilson, R.
                                                                                                                                                            Homo sapiens
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                                                        Williamson, A., Wohldmann, P. and
 version
replaced
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Best Local :
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GGGTCAGTGCAGAAGGTA 1248
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                                                                                                                                         TTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAA 1230
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/lab_host="DHIOB (ampicillin resistant)
/lab_host="DHIOB (ampicillin resista
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/db_xref="GDB:1267839"
/db_xref="taxon:9606"
/clone="IMAGE:342464"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="19 weeks"
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97.7%;
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Pred. No. 2.7e-94;
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                                                                                                                                                                                                                                                                                                                                                                                      Local
TTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATTTTCCCAAAA 1179
                                                                                                                  CGGGATAAGATCACCAGGCCAGGAGCGAANTANTGGAAGAAAGGGGAAGGGCTCCCCAAC 1119
                                                                                                                                                                   TCACTGGTGGGCTTTGAGATGNATATTACTCACTTGGATGGTCACAAGGTACATATTTCC 607
                                                                                                                                                                                                                                                                                                                                                             423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
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National Cancer Institute, Cancer Genome Anat
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NBHSF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002-150407, 151176-152327 Soares NBJHF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326380-32663 Soares NBHOT pool 1: 723720-726407, 73980-740999 Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soares and M. Fatima Bonaldo." 164 c 104 g 241 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:2364968"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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96.8%;
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Pred. No. 1.5e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACAGTTAACAGAGGAAGCGAGAAGGTATCAAACAGCTACTGAAACAAGGGTCAGTG 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTTCAATATGCAAGT 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be mede available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UI-M-BH2.2-aox-d-09-0-UI.sl NIH_BMAP_M_S3.2 Mus musculus cDNA clone UI-M-BH2.2-aox-d-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 443 1706 Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Forward POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9),
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                 /Strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.2-aox-d-09-0-UI"
/clone_lib="NIH_BMAP_M_S3.2"
/clone_lib="NIH_BMAP_M_S3.2"
/dev_stage="27-32 days"
/lab_host="PH10B (Life Technologies)"
/lab_host="PH10B (Life Tec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
   serially subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lennon, G. and Soares, M.B.
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Sciurognathi; Muridae; Murinae;
libraries were
generated in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bethesda,
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Mus.
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Query Match 30.2%; Score 415.4; DB 69; Length 480; Best Local Similarity 92.4%; Pred. No. 3.3e-92; Matches 437; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 GGCCCGCAGAACCTGAGCACCTTCTGCCTGTTGCTGCTGTACCTCATCGGGACTGTGAT 421
                                                                                                                                                                                                                           TAAAAAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGATCC 377
                                TTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACCAAACCTG 670
                                                                                                                                           TCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAGATCTAGAAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTGA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCGGGCGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCCATAAAGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCGGACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAAGGATAT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTCCGCAGAACCTGAGCACCTTTTGCCTGTTGCTGCTATACCTCATCGGGGCGGTGAT 257
                                                                                                                TCGTCAGCAGGACAGGAATATTCCAAGAGGAAGTGATATCATCGTAGATCTAGAAGTCAC
TCTGGAAGAAGTGTACGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      process: NIH_BMAP_M_S3.2, NIH_BMAP_M_S2, NIH_BMAP_M_S1.
The subtracted library (NIH_BMAP_M_S3.2) was constructed as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M_S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S3.2 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB-NIH_BMAP_M_S3.2
TAG_TISSUE-basal-ganglia
TAG_SEG-TGTAC."
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BASE COUNT ORIGIN

198

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Search completed: June 30, 2000, 12:12:13 Job time: 8064 sec

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819 120 558 180 498 240 438 300 378 360 318 420 258

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OM protein - protein search, using sw model
Run on:
                                                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score: US-09-501-714-1 1883

June 30, 2000, 09:57:25; Search time 40.12 Seconds (without alignments) 271.757 Million cell updates/sec

1 MAPQNLSTFCLLLLYLIGAV.....IKQLLKQGSVQKVYNGLQGY 358

Scoring table:

Searched: 83857 segs, 30454973 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
548 5 548 5 538 5 519 6 5 515 6 5 515 7 515 7 515 7 515 7 640 7	Score 1037.5
29.0 29.0 29.0 29.0 29.0 29.0 29.0 29.0	- CP TY
	Length DB
	1
DNJ'Z_ALLPO DNJH_ARATH DNJH_CUCSA DNJH_ATRNU DNJL_ALLPO DNJL_ALLPO DNJZ_HUMAN DNJZ_HUMAN DNJZ_HUMAN DNJZ_HUMAN DNAJ_ERUOV DNAJ_ACTAC DNAJ_ACTAC DNAJ_ACTAC DNAJ_COXBU HS41_HUMAN DNAJ_COXBU HS41_HUMAN DNAJ_COXBU DNAJ_TROCA DNAJ_TROCA DNAJ_TROCA DNAJ_FRACIU DNAJ_FRACIU DNAJ_FRACIU DNAJ_FRACIU DNAJ_FRACIU DNAJ_FRACIU DNAJ_FRACIU DNAJ_FRACIU DNAJ_BRCAP DN	ID
P42824 allium porr P42825 arabidopsis Q04960 cucumis sat P43644 atriplex nu Q03363 allium porr P31689 homo saplen P54102 mus musculu P25491 saccharomyc Q05980 brucella ov P08622 escherichia Q60004 salmonella P77866 actinobacit P71443 leptospira Q27352 methanobacit P42381 coxiella bu P25685 homo saplen Q04133 drosophila Q52702 rhodobacter P48208 haemophilus P30725 clostridium P40170 streptomyce P43735 haemophilus P30725 flasmonisella P35515 methanosarc P50025 legionella P34319 bradyrhizob Q9zdy0 rickettsia Q9zdy0 rickettsia Q92816 borrelia bu P07881 mycobacteri P39102 saccharomyc	Description Q10005 caenorhabdi

QΥ B δÃ DЬ δÃ

83

127 NIPRGSDIIVDLEVTLEEVYAGNEVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ 186

69 DLGAAYEVLSDSEKRKQYDTYGEEGL-KDGHQSSHG-DIFSHFFGDFGFMFGGTPRQQDR 126

DLSSAYEVLSDKEKRAMYDRHGEEGVAKMGGGGGGGHDPFSSFFGD--FFGGGGGHGGEE 125

Query Match 55.1%; Score 1037.5; DB 1; Length 355; Best Local Similarity 58.0%; Pred. No. 3.9e-78; Matches 203; Conservative 54; Mismatches 84; Indels 9;

Gaps

5.

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8 LIVLASSIVAFVECGRDFYKILGVAKNANANQIKKAYRKLAKELHPDRNQDDEMANEKFQ 67

366 19.4 379 1 DNAJ_LACLA 364.5 19.4 280 1 DNAJ_HETH 362.5 19.3 352 1 SIS1 YEAST 355 18.9 37.2 1 DNAJ_BACSU 354 18.8 528 1 YNAT_YEAST 351 18.6 404 1 SCJL_YEAST 348.5 18.5 370 1 DNAJ_ERYRH 344.5 18.3 352 1 DNAJ_STRPN 344.5 18.3 352 1 DNAJ_MYCGE 344.5 18.3 389 1 DNAJ_MYCLE 337.5 17.9 234 1 DNAJ_RHILE	19.4 2379 1 19.4 2379 1 19.3 352 1 18.9 372 1 18.6 404 1 18.5 370 1 18.3 352 1 18.3 389 1 18.3 389 1 17.9 234 1
379 1 280 1 352 1 372 1 404 1 370 1 352 1 389 1 389 1 234 1	379 1 DNAJ_LACLA 280 1 DNAJ_THETH 280 1 DNAJ_THETH 25294 372 1 SISI_YEAST 372 1 DNAJ_BACSU 528 1 YNH7_YEAST 404 1 SCJ1_YEAST 370 1 DNAJ_ERVRH 352 1 DNAJ_STRPN 352 1 DNAJ_MYCGE 389 1 DNAJ_MYCGE 389 1 DNAJ_MYCLE 334 1 DNAJ_MYCLE 33529
	1 DNAJ_THETH P35514 1 DNAJ_THETH Q56237 1 SIS1_YEAST P2594 1 DNAJ_BACSU P17631 1 YNH7_YEAST P53949 1 SCJ1_YEAST P5303 1 DNAJ_EYERH Q05646 1 DNAJ_STRPN P59830 1 DNAJ_MYCLE Q02605 1 DNAJ_RHILE Q33529
1 DNAJ_LACLA 1 DNAJ_HETH 1 SIS1_YEAST 1 DNAJ_BACSU 1 DNAJ_BACSU 1 SCJ1_YEAST 1 SCJ1_YEAST 1 DNAJ_ERYRH 1 DNAJ_STRPN 1 DNAJ_MYCGE 1 DNAJ_MYCLE 1 DNAJ_HILE	P35517 Q56237 P25594 P17631 P53903 P25303 Q05646 P95830 P95830 P95830 O2605 O23529
DNAJ_TACLA DNAJ_THETH SISL_YEAST SISL_YEAST DNAJ_BACSU YNH7_YEAST SCJI_YEAST DNAJ_ERYRH DNAJ_STRPN DNAJ_MYCGE DNAJ_MYCGE DNAJ_MYCHE	P35517 Q56237 P25594 P17631 P53903 P25303 Q05646 P95830 P95830 P95830 O2605 O23529

ALIGNMENTS

DR DR DR PFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	88888888	CCC RR RR R R CCC CCC	RESU YRY1 ID AC DT DT DT
EMBL; Z47356; CAA87414.1; HSSP; P08622; 1XBL. WORKPEP; T15H9.1; CE01664. PROSITE; PS00636; DNAJ_1; 1. PROSITE; PS0076; DNAJ_2; 1. PFAM; PF00226; DNAJ_C; 1. PFAM; PF01556; DNAJ_C; 1. Hypothetical protein; Chaperone; Signal. Hypothetical protein; Chaperone; Signal. SIGNAL 22 355 HYPOTHETICAL PROTEIN T15H9.1. CHAIN 22 355 HYPOTHETICAL PROTEIN T15H9.1. DOMAIN 97 103 POLY-GLY. DOMAIN 97 103 POLY-GLY. SEQUENCE 355 AA; 39861 MW; 95FA4D8E551D9CC2 CRC64;	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMME outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	T15H9:1. Caenorhabditis elegans. Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. [1] SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Gardner A.; SUBMILTED (JAN-1995) to the EMBL/GenBank/DDBJ databases.	1 년

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      Query Match
Best Local Similarity
Matches 126; Conser
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REPEAT
REPEAT
LIPID
SEQUENCE
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"Cloning of a new isoform of a DnaJ protein from Allium porrum
epidermal cells.";

Plant Physiol. Blochem. 32:723-727(1994).

-1- FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT PROBABLY
IN THE STRUCTURAL ORGANIZATION OF COMPARTMENTS (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).

-1- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR CXXCCGXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNJ2_ALLPO
P42824;
01-NOV-1995
01-NOV-1995
15-DEC-1998
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                                                                                                                                                                                                                             DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00637; DNAJ_CXXCXGXG; PROSITE; PS50076; DNAJ_2; 1. PFAM; PF00226; DNAJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P25685; 1HDJ.
PRINTS; PR00625; DNAJPROTEIN.
PROSITE; PS00636; DNAJ_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X77632; CAA54720.1; -. HSSP; P25685; 1HDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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hyta; Magnollophyta; Liliopsida; Asparagales;
      75;
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GLY-RICH.

CXXCXGXG MOTIF.

CXXCXGXG MOTIF.
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annotation
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Pred. No. 6.4e-38;
5; Mismatches 118;
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HSSP; P25685;
                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      COOKE R., LAUDIE M., RAYNAL M., Delseny M.;
SUBMITTED (MAR-1996) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT PROBABLY
IN THE STRUCTURAL ORGANIZATION OF COMPARTMENTS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
-!- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR CXXCCGXG
MOTIFS FOUND IN DNAJ PROTEINS.
                                                                                                                                                                                                                                              This
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
DNAJ PROTEIN HOMOLOG ATJ.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. COLUMBIA;
Zhou R., Hayman G.T., Kroczynska B., Miernyk J.A.;
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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PF00226; DnaJ; 1.
PF00684; DnaJ_CXXCXGXG;
PF01556; DnaJ_C; 1.
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                                             PR00625; DNAJPROTEIN.; PS00636; DNAJ_1; 1.; PS00637; DNAJ_CXXCXGXG; PS50076; DNAJ_2; 1.
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Q04960;
Q1-FEB-1994
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LIPID
CONFLICT
CONFLICT
SEQUENCE
                                                          *Plant dnaj homologue: molecular cloning, bacterial expres:
*Plant dnaj homologue: molecular cloning, bacterial expression analysis in tissues of cucumber seedlings.*;

Arch. Biochem. Biophys. 305:30-37(1993).

11. THE STRUCTURAL ORGANIZATION OF COMPARTMENTS.

11. THE STRUCTURAL ORGANIZATION OF COMPARTMENTS.

11. TISSUE SPECIFICITY: EXPRESSED IN SEEDLINGS IN ALL TISSUE SPECIFICITY: EXPRESSED IN SEEDLINGS IN ALL TISSUE SPECIFICITY: EXPRESSED IN SEEDLINGS AND ROOTS.

11. INDUCTION: WEAK, BY HEAT SHOCK.

11. SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR C.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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euphyllophytes; Caryophyllidae; Caryophyllales; Chenopodiaceae;
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PFAM; PF01556; DnaJ_C; 1.
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PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXXXG
PROSITE; PS50076; DNAJ_2; 1.
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BB4C0FE990561616 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNAJ-LIKE.
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                                                                                                        update)
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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      DNJ1_ALLPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
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REPEAT
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PFAM; PF00684; DnaJ_CXXCXGXG;
PFAM; PF01556; DnaJ_C; 1.
                                                                                                                                                                   308
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Zhu J.K., Shi J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVKPDQFKAIEDEGMPIYQRPFMKGKMYIHFTVEFP-DSLNPDQVKSLEAIL
                                                                                                                                                                                                     ITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLL
                                                                                                                                                                                                                                                                                                                                                                                                          Q-----EVV-----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLEDLFTGTTKKLSLSRNVICSKCTGKGSKSGASMKCSGCQGTGMKVSIRHLGPSMIQQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLEEVYAGNEVEV-VRNKPVARQAPGK------RKCN-CR---QEMRTTQLGPGRFQMT
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      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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GLY-RICH.

POLY-GLY.

CXXCXXXG MOTIF.

CXXCXXXG MOTIF.

CXXCXXXG MOTIF.

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Best Local S
Matches 124
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01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
01-NOV-1995 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chaperone;
NON_TER
DOMAIN
DOMAIN
DOMAIN
DOMAIN
REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00226; DnaJ; 1.
PFAM; PF00684; DnaJ_CXXCXGXG; PFAM; PF01556; DnaJ_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epidermal cells.";

FEBS Lett. 323:51-54(1993).

-I- FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT IN THE STRUCTURAL ORGANIZATION OF COMPARYMENTS.

-I- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).

-I- SIMILARITY: CONTAINS A DAMJ-LIKE DOMAIN AND THE FOUR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X69436; CAA49211.1; -. PIR; S31387; S31387. PIR; S33312; S33312. HSSP; P25685; 1HDJ.
           175
                                                       190
                                                                                                    115
                                                                                                                                               149
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Alliaceae; Allium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Asparagales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Occurrence and sequence of a DnaJ protein in plant (Allium epidermal cells.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bessoule J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 93265942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allium porrum (Leek).
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                                                                                                                                                                                             57
                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                       34 RSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQYDTYGEEG ::|| |:||||| |::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
{\tt GTGEMINDKDRCPLCKGEKVVQEKKVLEVHVEKGMQNGQRITFPGEADEAPDTVTGDIVF}
                       ---EVV-----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHVDGEPGDLRF
                                                                                                                                                                                                              LKDGHQSSHG-----DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEVTLEEVYAG
                                                                                        TSKKLSLSRNVICSKCNGKGSKSGASMRCASCQGSGMKVSIRQLGPGMIQQMQHPCNDCK
                                                                                                                                             NEVEVVRNKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOTIFS FOUND IN DNAJ PROTEINS.
                                                                                                                                                                                 LKEGMGGGGGDHDPFDIFQSFFGGGGFGGGGSSR--GRRQRRGEDVVHPLKVSLEELYNG
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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28, Last sequence update)
32, Last annotation update)
LOG 1 (DNAJ-1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prenylation; Lipoprotein; Multigene family
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66
87
134
150
177
193
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                                                                                                                                   -ARQAPGKRKCNCR---QEMRTTQLGPGRFQMTQ
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GLY-RICH.
CXXCXGXG |
CXXCXGXG |
CXXCXGXG |
CXXCXGXG |
                                                                                                                                                                                                                                                                                                                                                                     Score 519.5; DB 1;
Pred. No. 1.7e-35;
6; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FARNESYL (BY SIMILA
; 33BA6B981586EFAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNAJ-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTIF.
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  397;
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                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                        174
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                                           241
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RESULT 7
DNUZ_HUMAN
ID DNUZ_L HUMAN
ID DNUZ_L HUMAN
ID DNUZ_L DT 01-JUL
DT 01-OCT
DC Euther
RN EXQUEN
RX MEDLIN
RA Oh S.,
RT "Human
RI [2]
RN EXQUEN
RX MEDLIN
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Matches 133; Conser
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 93326630.
Oh S., Iwahori A., Kato S.;
"Human cDNA encoding DnaJ protein homologue.";
"Human cDNA encoding DnaJ protein homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNJ2_HUMAN
P31689;
                                                                                                                                                                                                                                                                                        PRINTS; PRO0625; DNAJPROTEIN.
PROSITE; PSO0636; DNAJ_1; 1.
PROSITE; PSO0637; DNAJ_CXXCXGXG;
PROSITE; PS50076; DNAJ_2; 1.
PFAM; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1174:111-113(1993).
-!- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR CXXCCGXG MOTIFS FOUND IN DNAJ PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chellaiah A., Davis A., Mohanakumar 1
"Cloning of a unique human homologue
heat shock protein.";
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01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
DNAJ PROTEIN HOMOLOG 2 (HSJ-2).
HSJ2 OR DNAJ2 OR HDJ2.
                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D13388; BAA02656.1; EMBL; L08069; AAC37517.1; PIR; S34631; S34631.
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Eukaryota; Metazoa; C
                                                                                                                                                           REPEAT
                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                          Chaperone;
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                                                                                                                                                                         REPEAT
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                                                                                                                                                                                                                                                          PF00684;
PF01556;
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                                                                                                                                                                                                                                                                                                                                                                                           P25685; 1HDJ.
                                                                                                                                                                                                                                          Repeat.
                                                                                                       75
134
150
177
193
274
                      Conservative
                                                                                                                                                                                                                                                   ; DnaJ; 1.
; DnaJ_CXXCXGXG;
; DnaJ_C; 1.
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96
141
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                                    27.4%;
34.5%;
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                      66;
                                                                                                   GLY-RICH.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
0 -> H (IN REF. 1).
0 -> H (IN REF. 2).
                                   Score 515.5;
Pred. No. 3.
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                      Mismatches
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                                    5; DB 1;
3.7e-35;
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                      117;
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                                                                                                       CRC64;
                                                    Length 397;
                      Indels
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                      69;
                   Gaps
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or send a
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MGD; MGI:1270129; HSJZ.
PRINTS; PR00625; DNAJPROTEIN.
PROSITE; PS00636; DNAJ_CXXCXGXG;
PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS50076; DNAJ_2; 1.
                                                                                     EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-MOUSE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P54102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNJ2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
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                                                                                     U53922; AAA98855.1;
P25685; 1HDJ.
                                                                                                                     AF055664; AAC78597.1;
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MEDLINE: 99017984.
Royaux I., Minner F., Goffinet A.M.,
Royaux II., Minner F., Goffinet A.M.,
"A DhaJ-like gene, Hsj2, maps to mou:
24 cM from the centromere.";
Genomics 53:415-415(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNAJ PROTEIN HOMOLOG 2 (HSJ-2).
BUAJ PROTEIN HOMOLOG 2 (HSJ-2).
HSJ2 OR DNAJZ OR RDJ1.
HSJ2 OR DNAJZ OR RDJ1.
Mus musculus (Mouse), and Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                             Leng C.H., Wang C.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR CXXCCGXG MOTIFS FOUND IN DNAJ PROTEINS.
                                                                                                                                                                                                                                                                                                               SPECIES=RAT; STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISR--DKI
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s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse
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                        (See http://www.isb-sib.ch/announce/
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RESQUENCE FROM N.A.

REDLINE; 91332099.

Caplan A.J., Douglas M.G.;

"Characterization of YDJ1: a yeast hopotein.";

J. Cell Biol. 114:609-67
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Matches 133
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01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MITOCHONDRIAL PROTEIN IMPORT PROTEIN MAS5 (PROT
MAS5 OR YDJI OR YNLÓS4C OR N2418 OR YNLÓS4C
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAS5_YEAST
P25491;
                                                                                                                                                                              "MAS5, a yeast import.";
                                                                                                                                                                                                                 MEDLINE; 92107179.
Atencio D.P., Yaffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEAST
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaperone;
DOMAIN
DOMAIN
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYDVLGVKPNATQEELKKAYRKLALKYHPDKNPNE---GEKFKQISQAYEVLADSKKREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETDEMDQVELVDFDPNQERRHYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLLKQGSVQKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKHGDIKCVLNEGMPIYRRPYEKGRLIIEFKVNFPENGFLSPDKLSLLEKLLPERKE-VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPK------EQLTEEAREGIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEEVYAGNFVEVVRNKPV----ARQAPGKR---KC--NCR---QEMRTTQLGPGRFQMTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPGDIIIVLDQKDHAVFTRRGEDLFMCMDIQLVEALCGFQKPISTLDNRTIVITSHPGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISR--DKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVCMECQGHGERISPKDRCKSCNGRKIVREKKILEVHIDKGMKDGQKITFHGEGDQEPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDTYGEEGLKDGHQ----SSHGDIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00226; DnaJ; 1. PF00684; DnaJ_CXX PF01556; DnaJ_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 34.5
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193
397
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                                                                                                                                                                                             homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                  M.P.;
log of DnaJ involved
                                                                                                                                                                                                                                                                                              Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
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GLY:RICH.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 515.5; DB 1
Pred. No. 3.7e-35;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378
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                                                        homologue
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                                                                                                                                                                                         mitochondrial protein
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                                                        of
                                                                                                                                                                                                                                                                                                          Saccharomycetales;
                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                        bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                        dnaJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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84 A8

86

YDTYGEEGLKDGHQSSHG---

-DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDII 135

65

26

7

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SOLUTION OF THE TARKEN SOLUTION OF THE TARKEN
          Query Match
Best Local Similarity
Matches 130; Conser
                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P25685; 1HDJ.

SGD; L0002503; YDJ1.

PRINTS; PR00625; DNAJ_1; 1.

PROSITE; PS00636; DNAJ_1; 1.

PROSITE; PS00637; DNAJ_CXXCXGXG; 1

PROSITE; PS00637; DNAJ_2; 1.

PRAM; PF00226; DNAJ_1.

PFAM; PF00264; DNAJ_CXXCXGXG; 1.

PFAM; PF01684; DNAJ_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; $74758; AAB20771.1; -.
EMBL; X56560; CAA39910.1; -.
EMBL; U12141; AAA99647.1; -.
EMBL; 271340; CAA95937.1; -.
PIR; A39659; A39659.
PIR; $36703; $26703.
                                                                                                                                                                                Repeat;
DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caplan A.J., Tsai J., Casey P.J., Douglas M.G.;
Francesylation of YDJ1p is required for function at elevated growth
temperatures in Saccharomyces cerevisiae.";
J. Biol. Chem. 267:18890-18895(1992).
1- FUNCTION: PROBABLY INVOLVED IN MITOCHONDRIAL PROTEIN IMPORT. IS
ALSO REQUIRED FOR EFFICIENT TRANSICATION OF PRE-PRO-ALPHA-FACTOR.
1- SUBCELLULAR LOCATION: CONCENTRATED IN A PERINUCLEAR RING AS WELL
AS IN THE CYTOPLASM (ACCORDING TO REF.2).
1- INDUCTION: MASS IS A HEAT SHOCK GENE WHOSE EXPRESSION INCREASES
MODERATELY AT ELEVATED TEMPERATURES.
1- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR CXXCCGXG
MOTHER FOUND IN DNAJ PROTEINS.
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                TIPID
                                                                                                                                                                                                                                                                                                                                                                       Chaperone; Heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergez P., Doignon F., Crouzet M.;
"The sequence of a 44 420 bp fragment located on chromosome XIV from Saccharomyces cerevisiae.";
Yeast 11:967-974(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERRATUM.
MEDLINE; 97060022.
Bergez P., Doignon F.,
Yeast 12:297-297(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288C / FY1
MEDLINE; 96021608.
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                                                                                                                                                                                                                                                                                                                                         Prenylation;
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  27.1%;
nilarity 36.6%;
Conservative 5
                                                                                                                                     406
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143
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150
166
192
208
                                                                                                                                     44670
                                                                                                                                                                                                                                                                                                                                         Lipoprotein
                                                                                                                                                                                                                                                                                                                                                               Transport;
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                                                                                                                                     ¥.
          56;
                                                                                                                             GLY-RICH.

CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
FARNESYL.
FARNESYL.
FARNESYL.
FARNESYL.
     Score 510; DB 1;
Pred. No. 1.1e-34;
5; Mismatches 119
                                                                                                                                                                                                                                                                                                                 DNAJ-LIKE.
                                                                                                                                                                                                                                                                                                                                                            Protein transport; Mitochondrion;
     119;
                                                  Length 409
                                                                                                                                   CRC64;
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     Indels
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     50;
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Gaps
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                                                  Chaperone;
                                                                                                                                                                                                                                                        This SWI
between
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                                DOMAIN
REPEAT
                                                                                                      HSSP; P08622; 1XBL.
PRINTS; PRO0625; DNAJPROTEIN.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q05980;
01-FEB-1994
  REPEAT
REPEAT
REPEAT
                                                                                                                                                         EMBL; M95799; AAC36133.1;
EMBL; M94063; AAA93047.1;
PIR; B47042; B47042.
                                                                                                                                                                                                                                                                                                                                                                                             Cellier M.F.M., Teyssier J., Nicolas M.,
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-ATCC 25840
                                                                                     PFAM;
                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                   use
                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of the Brucella ovis DnaK functionally expressed in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brucella ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNAJ_BRUOV
                                                                           PFAM;
                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                        Sri Widada J.;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93094135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                AK functionally expressed in Escherichia coli.";

Bacteriol. 174:8036-8042(1992).

FUNCTION: INVERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN
AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, J
WITH GRPE, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).

INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                       DNAJ-LIKE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPGEVIAPGMRKVIEGKGMP-IPKYGGYGNLIIKFTIKFPENHFTSE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAPDVIPGDVVFIVSERPHKSFKRDGDDLVYEAEIDLLTAIAGGEFALEHVSGDWLKVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGH--KVHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQRFQTECDVCHGTGDIIDPKDRCKSCNGKKVENERKILEVHVEPGMKDGQRIVFKGEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GRFQM-----TQEVV-----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGE
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                                                                                               PF00226; DnaJ;
                                                                           PF01556;
                                                                                    PF00684; DnaJ_CXXCXGXG; 1.
                                                                                                                                                                                                             non-profit institu
and this statement
requires a license
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(Rel.
(Rel.
  77
146
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199
                                                               replication;
                                                                          DnaJ_C;
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                                                                                                                                                                                                                                 institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last
Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
Heat shock;
DNAJ-LIKE.
GLY-RICH.
CXXCXGXG MC
CXXCXGXG MC
CXXCXGXG MC
CXXCXGXG MC
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Bardwell J.C.A., Georgopoulos C.;
"The nucleotide so
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15-DEC-1998
15-DEC-1998
                                                  Yura T., Mori H., Nagai
Isono K., Mizobuchi K.,
"Systematic sequencing
                                                                                                                                gene
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P08622;
                                                                                                                                                                                                           Ohki M. Tamura F., Nishimura S., Uchida "Nucleotide sequence of the Escherichia purification of the gene product.";
J. Biol. Chem. 261:1778-1781(1986).
                                               the
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                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria;
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STRAIN=K12 / MG1655;
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                                                                                                                        nucleotide sequence of the Escherichia that encodes a heat shock protein."; iol. Chem. 261:1782-1785(1986).
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Pred. No. 2.3e-31;
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PRINTS; PRO0625; DNAJEROTEIN.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PFAM; PF00226; DnaJ; 1.
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J. Mol. Biol. 260:236-250(1995).
-!- FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN OF THE PHAGE LAMBDA ORIGIN OF REPLICATION. STINULATES, JUNIT HE ATPASE ACTIVITY OF DNAK.
-!- SUBUNIT: HOMODIMER.
-!- SUBUNIT: HOMODIMER.
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ECO2DBASE; H036.5; 6TH EDITION.
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S40537; S40537.
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SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND
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PRINTS; PRO0625; DNAJPROTEIN.
PROSITE; PSO0635; DNAJ-1; 1.
PROSITE; PS50076; DNAJ-2; 1.
PROSITE; PS00637; DNAJ-CXXCXGXG;
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, J. WITH GRPE, THE ATPASE ACTIVITY OF DNAK.

-I- SUBUNIT: HOMODIMER (BY SIMILARITY).

-I- INDUCTION: BY HEAT SHOCK UNDER THE CONTROL OF THE HTPR INDUCTION: BY HEAT SHOCK UNDER THE CONTROL OF THE HTPR INDUCTION:
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PFAM; PF00684; DnaJ_CXXCXGXG;
PFAM; PF01556; DnaJ_C; 1.
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"Actinobacillus actinomycetemcomitans.";
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FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN COMPLEX AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY WITH GREE, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).

SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND TO EUKARYOTIC DNAJ-LIKE PROTEINS.
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                                                                                                                                                           Usage
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DNAJ_LEPIN
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Best Local S
Matches 123
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         Gul B., Yelton D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN COMPLEX AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY WITH GREE, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).
-!- SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND TO EUKARYOTIC DNAJ-LIKE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
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REPEAT
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PFAM; PF00684; DnaJ_CXXCXGXG;
PFAM; PF01556; DnaJ_C; 1.
                                                                                                                                                                           SEQUENCE FROM N
STRAIN-WIJNBERG
                                                                                                                                                                                                                                     DNAJ
                                                                                                                                                                                                                                                      15-JUL-1998 (Rel.
15-FEB-2000 (Rel.
15-FEB-2000 (Rel.
                                                                                                                                "Molecular analysis of serovar Copenhageni.";
                                                                                                                                                       Ballard
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                                                                                       STRAIN-SEROTYPE
                                                                                                  SEQUENCE OF 1-35 FROM
                                                                                                                       Gene
                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                              DNAJ PROTEIN.
                                                                                                                                                                                                                                                                                          P71443;
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                                                                                                                                                                                                                        Leptospira
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
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hes 123;
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                                                                                                                       216:21-29(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDS :| :|:|::|: || || ||:| ||:| || ||:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAKQDYYELLGISRSADEKEIKRAYKKLAMQYHPDRTKGDKEKEEKFKEIQEAYEVLNDK
                                                                                                                                                                                                                                                                                                                                                           LKIPEETQTGKLFRMRGKGVTS-TRSGYAGDLTCRIIVETP-VKLNEEQKELLRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGPGREQMTQ------EVVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDLEVTLEEVYAGNFVEVVRNKPVARQAP------GKR-----KCNCRQEMRTTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKRKQYDTYG----EEGLKDGHQSSHGDIFSHFFGD-FGFMFGGTPRQQDRNIPRGSDII
                                                                                                                                                                                                                                                                                                                                                                                 ISRDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQL
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                                                                                                                                                      S.A.,
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                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                     POMONA;
                                                                                                                                                                                                                                                        39,
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152
169
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Last annotation update)
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                                                                                                                                            S R.P.A.M.,
dnaK locus
                                                                                                                                                                                                            Leptospiraceae;
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CXXCXGXG
CXXCXGXG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat shock;
DNAJ-LIKE.
GLY-RICH.
CXXCXGXG MO
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Pred. No. 1.6e-29;
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of Lep
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                                                                                                                                             interrogans
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Best Local Similarity
                                                                                                           DNAJ_METTH
027352;
15-JUL-1998
15-JUL-1998
15-JUL-1998
                                               Methanobacterium thermoautotrophicum Archaea; Euryarchaeota; Methanobacte: Methanobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
SEQUENCE
                                                                                     DNAJ PROTEIN.
DNAJ OR MTH1291.
STRAIN-DELTA
MEDLINE; 9803
                      SEQUENCE FROM N.A.
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Chaperone; DNA replication; Heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                     LLKQ-----
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                                                                                                                                                                                                                                                                               GKKAKMKIPEGTESGQVFRLKGHGMPYLGAYG-KGDQHVIVKIEIPK-KITRRQRELIEE
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                                                                                                                                                                                                                                                                                                                                                                                 SGQIRRTQGFFSVATTCPTCRGKGTIISNPCRSCGGQGLQEKRRTINIKIPPGVETGSRL
                                                                                                                                                                                                                                                                                                                                                                                                        SDIIVDLEVTLEEVYAGN--FVEVVR-----NKPVARQAPGKRKC-NCRQEMRTTQLG
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U72647; AAB17396.1;
P08622; 1XBL.
                                                                                                            (Rel. 36, Created)
(Rel. 36, Last seq
(Rel. 36, Last ann
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167
189
203
369 ;
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39939 .
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                                                                                                                                                                                                                                                     352
                                                             Methanobacteriales;
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                                                                                                            sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches
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CXXCXGXG MOTIF.

CXXCXGXG MOTIF.

CXXCXGXG MOTIF.

CXXCXGXG MOTIF.

CXXCXGXG MOTIF.
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Pred. No. 4.1e-29;
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shock; Repeat.
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                                                                                                                        update)
                                                                                                                                                               376
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                                                           Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
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                                                                                                                                                                                                                                                                                                                              292
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A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
A Daniels G.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
T Complete genome sequence of Methanobacterium thermoautotrophicum
GeltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
C -i- FUNCTION: STIMULARIES, JOINTLY WITH GRPE, THE ATPASE ACTIVITY OF
DNAK (BY SIMILARITY).
               Query Match
Best Local
   Matches 126;
                                                                          REPEAT
SEQUENCE
                                                                                                                      DOMAIN
REPEAT
REPEAT
                                                                                                                                                                  Chaperone;
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      HSSP; P08622; 1XBL.
PRINTS; PR00625; DNAJ_PROTEIN.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS0076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                        REPEAT
                                                                                                                                                                                                 PFAM;
               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNAJ-LIKE PROTEINS.
                                                                                                                                                                                              PF00226;
PF00684;
PF01556;
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                                                                                                                                                                                  DNA
 Conservative
                                                                                                                                                                             DnaJ; 1.
DnaJ_CXXCXGXG; 1.
DnaJ_C; 1.
replication; Heat shock;
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                                                                        71
118
155
172
198
212
41584 MW;
               23.4%;
 55;
                                                                      CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXXGXG MOTIF.
CXXCXXGXG MOTIF.
              Score
Pred.
                                                                                                                                                  DNAJ-LIKE.
GLY-RICH.
 Mismatches
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                                TLD-RPVKLRIPAGTQSGTTFRVKGHGMPHLKWNGY-GNLYVKVKVVTPRKLSPRQ----
                                                           HLDGHKVHISRDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREG
                                                                                          SRLRVPGEGEMGLRGGEPGDLYVVIKVKPHSIFRREGANLYTEKPISFVQAALGDTVEVP
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Search completed: June 30, 2000, 11:56:22 Job time: 7137 sec

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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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Qy 13 LLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLAKQLHPDRNPDDPQAQEKFQ 68	RESULT 1 T24938 RESULT 1 T24938 hypothetical protein T15H9.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Accession: T24938 R; Gardner, A. Sumitted to the EMBL Data Library, January 1995 A; Reference number: Z19958 A; Accession: T24938 A; Accession: T24938 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-355 <wil> A; Cross-references: EMBL:247356; PIDN:CAA87414.1; GSPDB:GN00020; CESP:T15H9.1 A; Experimental source: clone T15H9 C; Genetics: A; Gene: CESP:T15H9.1 A; Apap position: 2 A; Introns: 42/3; 74/3; 129/3; 151/3; 208/3; 249/2; 290/3 A; Introns: 42/3; 74/3; 129/3; 151/3; Pred. No. 2.8e-79; Best Local Similarity 58.0%; Pred. No. 2.8e-79; Matches 203; Conservative 54; Mismatches 84; Indels 9; Gaps</wil>	31 406 21.6 392 2 G72128 heat shock protein 32 405.5 21.5 389 2 S41748 heat shock protein 33 403 21.4 369 2 B73327 dnaJ protein - The 34 401 21.3 392 2 G71726 dnaJ protein - The 35 392.5 20.8 498 2 T05590 dnaJ protein (dnaJ 37 390.5 20.7 379 2 S55900 heat shock protein 38 390.5 20.7 379 2 S75590 heat shock protein - fiss 39 389.5 20.7 378 2 S72590 hp. and protein - fiss 39 389.5 20.7 378 2 S72590 hp. and protein - fiss 37 390.5 20.6 382 2 D70587 hp. and protein - fiss 39 389.5 20.4 364 2 D70587 hp. and protein - fiss 377.5 20.0 352 2 A49210 heat shock protein - fiss 377.5 20.0 413 2 T40427 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133 heat shock protein - fiss 369.5 19.6 336 2 T09133
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RESULT 2 \$71199 dnaJ protein homolog atj3 - Arabidopsis thaliana

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LDJ2 protein - leek

C; Species: Allium porrum (leek)

C; Species: 06-Jan-1995 *sequence_revision 06-Jan-1995 *te

C; Caccession: S42031

R; Bessoule, J.J; Testet, E; Cassagne, C.

submitted to the EMBL Data Library, February 1994

A; Reference number: S42031

A; Recession: S42031

A; Accession: S42031

A; Accession: S42031

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-418 <BES>

A; Residues: 1-418 <BES>
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C;Superfamily: heat shock protein dnaJ; dnaJ
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Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 20-Aug-1999
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                                         YYEVLGVSKNATPEDLKKAYRKAAIKNHPDKGGD----PEKFKEIGQAYEVLNDPEKREI 69
                                                               FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ 85
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YDTYGEEGLKDGHQSSHG-----DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEV
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                                                                                                                        29.2%; Score 549.5; DB 2; 35.0%; Pred. No. 2.4e-38; Live 75; Mismatches 118;
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Pred. No. 1.8e-38;
'1; Mismatches 118
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A; Molecule type: mRNA
A; Residues: 1-223, 'V', 225-239, 'A', 241-302, 'P', 304-377, 379-380, 'V', 381-413
A; Cross-references: EMBL: X67695; NID: 918259; PIDN: CAA47925.1; PID: 918260
C; Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F; 12-73/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X67695
R;Prelsig-Mueller, R.; Kindl, H.
submitted to the EMBL Data Library, August 1992
A;Description: Plant equivalent of a nuclear loc
A;Reference number: S31414
A;Accession: S31414
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A; Residues: 1-413 < PRE1>
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Arch. Biochem. Biophys. 305, 30-37, 1993
A;Title: Plant dnaJ homologue: molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Cucumis sativus (cucumber)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
C;Accession: S35581; S31414
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      13 YYEILGVSKNASQDDLKKAYRKAAIKNHPDKGGD----PEKFKELAQAYEVLSDPEKREI 68
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                                                                                                                                                                                                                                                       LEEVYAGNE -- VEVVRN----- KPVARQAPGKRKC-NCR--- QEMRTTQLGPGREQMTQ
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TRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEE--AREGIKQLLKQGSVQ
                                          VTGDIVFVLQQKEHPKFKRKGDDLFVEHTLSLVESLCGFQFILTHLDGRQLLIKSLRGEV
                                                                                EPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHIS--RDKI 292
                                                                                                                              HPCNECKGTGETINDKDRCSQCKGEKVVQEKKVLEVIGEKGMQNAQKITFPGERDEAPDT
                                                                                                                                                                                                                                                                                                                                           YDTYGEEGLKDGHQSSHG----DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEVT 141
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RESULT 6
J02142
Chaperone ANJ1 protein - Atriplex nummularia
C;Species: Atriplex nummularia
C;Species: Atriplex nummularia
C;Species: Atriplex nummularia
C;Species: Atriplex nummularia
C;Bate: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 05-Dec-1997
C;Accession: J02142
R;Zhu, J.K.; Shi, J.; Bressan, R.A.; Hasegawa, P.M.
Plant Cell 5, 341-349, 1993
A;Title: Expression of an Atriplex nummularia gene encoding a protein homol A;Reference number: J02142; MUID:93222693
A;Accession: J02142
A;Molecule type: mRNA
A;Residues: 1-417 <ZHU>
A;Cross-references: GB:L09124
C;Comment: This protein is involved in protein folding and is observed as h C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T07371
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-419 < LEG>
A; Cross-references: EMBL: X94301; NID: 91125690; PIDN: CA
A; Experimental source: tissue type leaf
C; Genetics:
A; Gene: dnaJ
A; Note: induced upon tuberization
C; Superfamily: heat shock protein dnaJ; dnaJ amino-ter
C; Keywords: molecular chaperone
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T07371
dnaJ protein homolog - potato
C.Species: Solanum tuberosum (potato)
C.Date: 14-May-1999 #sequence_revision 14-May
C.Accession: T07371
R:Leggewie, G.; Braun, H.P.
Plant Physiol. 117, 1127, 1998
A:Title: A cDNA from potato with homology to
A:Reference number: Z15992
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ss: Solanum tuberosum (potato)
14-May-1999 #sequence_revision 14-May-1999
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C;Species: Al
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A; Residues: 1-397 <BES>
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;Date: 06-Jan-1995 #sequ
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Best Local :
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Best Local Similarity
Matches 123; Conser
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     RIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISRD--KITRPGAXX
                                                                                                                                        NEVEVVRNKPV-----

    leek (fragment)

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                                                                                                                                                                                                                                                                                                           Conservative
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A; Gene: dnaJ
C; Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;1-53/Domain: dnaJ amino-terminal homology (fragment) <DNJ>
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                                                                                                                                                                                                                                                                                                    34 RSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEYLSDSEKRKQYDTYGEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 YYEILGVPKDASPEDLKKAYKKAAIKNHPDKGGD----PEKFKELAHAYEVLSDPEKREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLL
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GTGEMINDKDRCPLCKGEKVVQEKKVLEVHVEKGMQNGQRITFPGEADEAPDTVTGDIVF
                                                                                                                                                                                                                                                                              KNASPDDLKKAYRKAAIKNHPDKGGD----PEKFKELAQAYDVLSDPEKREIYDQYGEDA
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                                                                                                                                                                                  LKDGHQSSHG-----DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEVTLEEVYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVKPDQFKAIEDEGMPIYQRPFMKGKMYIHFTVEFP-DSLNPDQVKSLEAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVTGDTVFVLQQKEHPKFKRKGEDLFYEHTLSLTEALCGFRFVLTHLDGRQLLIKSNLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISRD--K
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                                           ---EVV-----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHVDGEPGDLRF
                                                                                       TSKKLSLSRNVICSKCNGKGSKSGASMRCASCQGSGMKVSIRQLGPGMIQQMQHPCNDCK 174
                                                                                                                                  -ARQAPGKRKCNCR---QEMRTTQLGPGRFQMTQ-----
                                                                                                                                                                                                                                                                                                                                                                                             Score 519.5; DB 2
Pred. No. 7.2e-36;
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Pred. No. 2e-36;
0; Mismatches 118;
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DnaJ protein
C; Species: Ze
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A;Residues: 1-273, 'H', 275-397 <IWA>
A;Residues
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A; Residues: 1-397 < CHE>
A; Residues: 1-397 < CHE>
A; Cross-references: EMBL:L08069; NID:g306713; PIDN:AAC37517.1;
A; Cross-references: umbilical vein endothelium
A; Ch, S: Iwahori, A: Kato, S.
Blochim. Blophys. Acta 1174, 114-116, 1993
Blochim. Blophys. Acta 1174, 114-116, 1993
A; Title: Human CDNA encoding DnaJ protein homologue.
A; Reference number: S34631; MUID:93326630
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #seguence_revision 06-Jan-1995
C;Accession: S34630; S34631
R;Chellalah, A.; Davis, A.; Mohanakumar, T.
Blochim. Blophys. Acta 1174, 111-113, 1993
A;Title: Cloning of a unique human homologue of the A;Reference number: S34630; MUID:93326629
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                                                                                                                                                                                       ETDEMDQVELVDFDPNQERRRHYNG
                                                                                                                                                                                                                                                                                                           VKHGDIKCVLNEGMPIYRRPYEKGRLIIEFKVNFPENGFLSPDKLSLLEKLLPERKE-VE
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                             ZMDJ1
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Pred. No. 1.6e-35;
6; Mismatches 117;
                                                                                                                                                                                       378
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dnaJ protein homolog YDJ1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: dnaJ protein homolog MAS5; protein N2418; protein YNL064.
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Aug-1999
C;Accession: S26703; A39659; S58714; S62992; S17250
R;Atencio, D.P.; Yaffe, M.P.
Mol. Cell. Biol. 12, 283-291, 1992
A;Reference number: S26703; MUID:92107179
A;Accession: S26703; MUID:92107179
                                                                                            A; Title: Characterization of YDJ1: a yeast A; Reference number: A39659; MUID:91332099 A; Accession: A39659
R;Bergez, P.; Doignon,
Yeast 11, 967-974, 1995
            A;Cross-references: GB:x56560; NID:g4810; PIDN:CAA39910.1; R;Bergez, P.; Doignon, F.; Crouzet, M.
                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-409 <ATE>
A;Cross-references: GB:S74758; NID:g241522; PIDN:AAB20771.1;
                                                      A;Residues: 1-409 <CAP>
                                                                      A; Molecule type: DNA
                                                                                                                                                   R;Caplan, A.J.; Dou
J. Cell Biol. 114,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 19-Feb-1999 #sequence_revi
C;Accession: T01643
R;Baszczynski, C.L.; Barbour, E.;
Maydica 42, 189-201, 1997
A;Title: Characterization of a gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: Z14364
A;Accession: T01643
A;Status: preliminary; translated
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D--KITRPGAXXWKKGEGLPNFDNNNIKGSLITTFDVDFPKEQLTEEAR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAPDTVTGDIVFVLQQKDHSKFKRKGEDLFYEHTLSLTEALCGFQFVLTHLDNRQLLIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPGEVVKPDQFKAINDEGMPIYQRPFMKGKLYIHFTVEFPDSLAPEQCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDQYGEDALKEGMGGGGSHVDPFDIFSSFFGPSFG----GGGGSSRGRRQRRGEDVVHPLK 126
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                  PID:g4811
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submitted to the EMBL Data Library, June 1998
A; Description: Isolation and characterization of a Dna
A; Reference number: Z16649
A; Accession: T09338
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-423 <FRU>
A; Cross-references: EMBL:AF069507; NID:g3202019; PID:g
C; Genetics:
A; Gene: MsJ1
A; Introns: 51/3; 108/1; 155/2; 200/1; 247/3; 314/1
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A;Accession: $58714
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-409 <BER>
A;Cross-references: EMBL:U12141; NID:g1314216; PIDN:AAA99647.1; PID:g994823
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: $62975
A;Accession: $62992
A;Molecule type: DNA
A;Residues: 1-409 <BEN>
A;Residues: 1-409 <BEN>
A;Residues: 1-409 <BEN>
A;Residues: SEMB:Z71340; NID:g1301940; PIDN:CAA95937.1; PID:e239683; PID:g130194
A;Experimental source: Strain $288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 14L c; Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology C; Superfamily: heat shock; mitochondrion; stress-induced protein E; 6-70/Domain: dnaJ amino-terminal homology CDNJ>
                                                                                                                                                                                                                                                                                             DnaJ-like protein MsJ1 - alfalfa
C; Species: Medicago sativa (alfalfa)
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
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T09338
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R; Frugis, G.; Mele,
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A;Cross-references: SG
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                                                                                                                                                                                                                                                   G.; Mele, G.; Giannino, D.; Mariotti, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDLEVTLEEVYAGNFVEVVRNKPV-ARQAPGK----RKC-NCRQE---MRTTQLGP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDTYGEEGLKDGHQSSHG-------DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDII 135
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                                                                          PID: g3202020
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision
C;Accession: T31734
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A; Residues: 1-439 <BLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Blanchard, M.; Bradshaw, H.; Kramer, J. submitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cosmid T05C3
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                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:T05C3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain Bristol N2; clone T05C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T31734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T05C3.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
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Best Local :
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                                                                                                                                                                                                                                      15 YTTLNVRPDASQADIKKSYFKLAKEYHPDKNPDH----GDKFKEISFAYEVLSSPEKRRLY 71
                                                                                                                                                                                                                                                                   27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEYLSDSEKRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                   YKILGYPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISRD-
| ||: | ::| || | | | ||: ::| ||: ::|||| :: :
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                                                                                                            GGPRRR-----KFQDTVHPLNVTLEELYVGKTSKLKLSKKALCKTCEGSGGKKGEKYKCD
                                                                                                                                         --PROODRNIPRGSDIIVDLEVTLEEVYAGNFVEV-VRNKPVARQAPG-----KRKCN 170
                                                                                                                                                                                            DTYGEEGLKDGHQSS-----HGDIFSHFFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEVIKPGQHKAINDEGMPQHGRPFMKGRLYIKFSVDFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTQEVV-----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPH 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVTLEEVYAGNEVEV-VRNKPVARQAPGK-----RKCNCR---QEMRTTQLGPGRFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DARGLEGYQGGGAGGGGGFPGGLFSHFFGGAGGDDDDDDDDDDDGGHPFGGLFGGMGGMGR 131
                                               ACRGRGVKTIVQQIGPGMLQQMQ-VHCDACKGSGGKVPAGDKCKGCHGEKYENVSKILEV
                                                                               -CR-QEMRT--TQLGPGRFQMTQEVVCDECP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121;
                                                                                                                                                                                                                                                                                                                                                                              267/3; 298/2;
                                                                                                                                                                                                                                                                                                                  Similarity
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35.0%;
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35.8%;
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                                                                                                                                                                                                                                                                                                             Score 495; DB 2;
Pred. No. 9.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 507.5; DB Pred. No. 8e-35; 7; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN: AAB65361.1;
                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                         -----DFGFMFGGT----
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                                                                                                                                                                                                                                                                                                    116;
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                                                                             ----NVKLVNEERTLEV
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T22648
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C;Superfamily: |
F;8-72/Domain: (
hypothetical protein F54D5.8 - Caenorha
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T22648
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A; Molecule type: DNA
A; Residues: 1-376 < AQF>
A; Cross-references: GB:AE000703; NID:g2983287; PIDN:AAC06881.1; PID:g2983289; GB:AE00065
A; Experimental source: strain VF5
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Aug-1999
C;Accession: E70381
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E70361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666 A;Accession: E70361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.0
Best Local Similarity 34.5
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                     353 GKK-VEELLKQ
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                                                                                                                                                                                                                                HLDGHKVHISRDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPK----EQLTEE
                                                                                                                                                                                                                                                                                                                                                                    MRTTQLGPGRFQMTQEVVCDECPNVKLVNE------ERTLEVEIEPGVRDGME
                                                                                                                                                                     AREGIKQLLKQ 345
                                                                                                                                                                                                  TLDGEKVKVKIPPGTKEGELIKVPGKGMPRLKGSG-RGDLYVRVHIDVPKIGVLSKLLGD
                                                                                                                                                                                                                                                                                                                                    GETVQ-GNWFFQVRQ--TCPTCGGEGVIYENCHACTGRGYGLVKETIKVKIPPGVRDGSK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQYDTYGEEGLKDGHQSSHG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKR 83
                                                                                                                                                                                                                                                                     --LVVEGKGHAGRYGGPPGDLYIIVKVKPHKIFERKGDDLYVDVNITYPEAVLGTEVEVP
                                                                                                                                                                                                                                                                                       RRRRSVKGEDIVVPVEITLEEAFKGTTVPIEVEREVPCSACGGTGYDESKSRTCPTCGGR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLYDMY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVLPGMKHNDKITFKGDGDQSDPDGEPGDVVIVIQQKDHDIFKRDGDDLHMTKKLSLNEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein dnaJ; dnaJ amino-terminal homology dnaJ amino-terminal homology <DNJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GHAAFEGAGAQQRVETTEIPPIEEILREFFDFDIGSIFERATGRRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.0%; Score 490; DB 2; 34.5%; Pred. No. 2e-33; tive 61; Mismatches 118

    Caenorhabditis elegans

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              15-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118;
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heat shock protein dnaJ - Brucella ovis
C;Species: Brucella ovis
C;Species: Brucella ovis
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: B47042
R;Cellier, M.F.; Teyssier, J; Nicolas, M.; Liautard, J.P.; Marti, J.; Sri v
J. Bacteriol. 174, 8036-8042, 1992
A;Title: Cloning and characterization of the Brucella ovis heat shock prote.
A;Reference number: A47042; MUID:93094135
A;Accession: B47042
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-375 CCEL>
A;Molecule type: nucleic acid
A;Residues: 1-375 CCEL>
A;Residues: 1-375 CCEL>
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology C;Keywords: DNA replication; heat shock; molecular chaperone F;4-69/Domain: dnaJ amino-terminal homology <DNJ> F;76-108/Region: GF motif F;146-153/Region: CXXCXGXG repeat F;163-170/Region: CXXCXGXG repeat F;185-192/Region: CXXCXGXG repeat F;185-192/Region: CXXCXGXG repeat
                                                                                                                                                                                  A; Note: sequence C; Genetics:
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submitted to the EMBL Data Library, October 1995
A;Reference number: Z19593
A;Accession: T22648
A;Accession: T22648
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-331 <WIL>
A;Residues: 1-331 <WIL>
A;Cross-references: EMBL:Z66513; NID:e1062016; PIDN:CAA91334.1; GSPDB:GN00020; CESP:F
A;Experimental source: clone F54D5
C;GenetLCS:
C;GenetLCS:
A;Genet: CESP:F54D5.8
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NCBI backbone
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Pred. No. 7.1e-32;
i5; Mismatches 102;
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F;199-206/Region: CXXCXGXG repeat
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Search completed: June 30, 2000, 09:58:19 Job time: 939 sec

Run on

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Post-processing: Minimum Match 0%
Listing first 45 summaries
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              US-09-388-93-3

US-08-868-288A-7

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US-08-897-240-34

US-08-879-260-4

US-08-879-260-4

US-08-346-849-12

US-08-346-849-12

US-08-346-849-10

US-08-346-849-10

US-08-346-849-9

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US-08-868-288A-1
                        Query Match
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Matches 358; Conserv
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                                                                                                                        TOPOLOGY: line
IMMEDIATE SOURCE:
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OPERATING SYSTEM:
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CITY: Palo Alto
STATE: CA
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Result No.

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ALIGNMENTS

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Sequence 1, Application US/08868288A Patent No. 5922567
                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UFILING DATE: June 3, PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Au-Young, Janice
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE
                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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Score 1879; DB 2;
Pred. No. 2.3e-199;
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Mismatches

Length 358; Indels

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US-09-235-373-1
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                                                                 US-09-235-373-1
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
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APPLICANT:
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APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                          TOPOLOGY: line
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                          FILING DATE: June 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                             LIBRARY: SYNO)
CLONE: 136466
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                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                            LENGTH:
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                                                                                              SYNORAB01
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99.8%;
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Score 1879; DB 3; pred. No. 2.3e-199;
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               Length 358;
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US-09-388-993-1
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                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 358 amino acid
                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                         IMMEDIATE SOURCE:
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    MMEDIA: SINCE
LIBRARY: SINCE
TONE: 136466
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CITY: P
                                                     TOPOLOGY:
                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
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                                                                                                 358 amino acids
                                                                                                                                            415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Au-Young, Janice
                             SYNORAB01
                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08868288A
Patent NO. 5922567
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 358;
                                             TELEPAX: 415-843-34-10 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: 1397 amino acids
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08 FILING DATE: June 3, 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
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                          TYPE: amino a STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
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                TOPOLOGY:
                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                          amino acid
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3174 Porter Drive
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             linear
                               single
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100.0%; Pr
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Pred. No. 2.3e-199;
                                                                                                                                                        pr-0309 US
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US-08-868-288A-5
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Best Local Similarity
Matches 133; Conserv
                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/868,281
FILING DATE: June 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Au-Young, Janice
APPLICANT: Lal, Preett
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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: CA
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3174 Porter Drive
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                   415-845-4166
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RESULT 6
US-09-388-993-5
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Best Local Similarity 34.5
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Au Young, Janice
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                            APPLICATION NUMBER: US/09/388,993
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/868,288
                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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LIBRARY: GenBa
CLONE: 306714
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LENGTH: 397 amino acids
                                                                                                                           COMPUTER: IBM CON
OPERATING SYSTEM:
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                  FILING DATE
                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 YDKGGEQAIKEGGAGGGFGSPMDIFDMFFG-----GGGRMQRER----RGKNVVHQLSVT
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STRANDEDNESS: si
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Sequence 3, Application US/08686417
Patent No. 5850018
GENERAL INFORMATION:
APPLICANT: Baszczynski, Chris
APPLICANT: Barbour, Eric
APPLICANT: Barbour, Eric
APPLICANT: Horowitz, Jeannine
APPLICANT: Rosichan, Jeffrey L.
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Best Local Similarity
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ZIP: ZUVVU III.
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPORTER: IBM PC compatible
                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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IMMEDIATE SOURCE:
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                                                                                                 STREET: 2000 Pen
CITY: Washington
STATE: DC
                                                              COUNTRY: USA
ZIP: 20006-1888
                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKHGDIKCVLNEGMPIYRRPYEKGRLIIEFKVNFPENGFLSPDKLSLLEKLLPERKE-VE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDKGGEQAIKEGGAGGGFGSPMDIFDMFFG-----GGGRMQRER---RGKNVVHQLSVT 114
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                                                                                                                                 E: MORRISON & FOERSTER 2000 Pennsylvania Avenue,
                                                                                                                                                                                                     HOTOWITZ, Jeannine
Rosichan, Jeffrey L.
VENTION: AN EXPRESSION CONTROL SEQUENCE FOR
VENTION: GENERAL AND EFFECTIVE EXPRESSION OF GENES
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34.5%; Pred. No. 1.2e
ative 66; Mismatches
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1.2e-48;
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US-08-974-546-1
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                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08974546 Patent No. 5945287
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                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                            TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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LENGTH: 419 amino acids
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REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 QMTQEVVCDECPNV--------KLVNEERTLEVEIEPGVRDGMEYPFIGEGE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 D--KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 EAPDTVTGDIVFVLQQKDHSKFKRKGEDLFYEHTLSLTEALCGFQFVLTHLDNRQLLIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 VTLEEVYAGNFVEVVRNKPV-------ARQAPGKRKCNCRQEMRTTQLGPGRF 185
                                                                                                                                STREET: 3174 POI
CITY: Palo Alto
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COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 YYEILGVPKSASQDDLKKAYRKAAIKNHPDKGGD----PEKFKELAQAYEVLSDPEKREI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ 85
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                                                                                                                                                                                                                                                                                                                      Jennifer L.
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RESULT 9
US-08-974-546-5
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                                                                                                                                                                                 Sequence 5, Application US/08974546 Patent No. 5945287
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                    APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 6
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APPLICATION NUMBER:
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LIBRARY: BALL
TONE: 2525691
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REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                             IVEFKVRFP-DRLTPQTRQILKQHL 345
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; Pred. No. 2.6e-41;
61; Mismatches 100;
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COUNTRY:

USA

Palo Alto 94304

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; CLONE: 1816452
US-08-974-546-5
          Sequence 6, Application US/08472534
Patent No. 5919620
GENERAL INFORMATION:
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TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
APPLICANT:
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IMMEDIATE SOURCE:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650-855-0555
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
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                                                                                                                            321 IFP-ERIPQTSRTVLEQVL 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 RKQYDTYGEEGLKDGHQSS-------HGD---IFSHFFG---DFGFMFGGTP 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 GRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
mes 114; Conserv
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STRANDEDNESS: si
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                                                                                                                                                             DFPKEQLTEEAREGIKQLL 343
                                                                                                                                                                                                                         SLVESLVGFEMDITHLDGHKVHISRDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDV 324
                                                                                                                                                                                                                                                                              ---QRNGEEGMDIDDPFSGFPMGMGGFTNVNFGRSRSAQEPARKKQDPPVTHDLRVSLEE 174
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30.1%; Pred. No. 4.6e-40;
tive 59; Mismatches 106;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brodeur, APPLICANT: Martin, I TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: Bi
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
339 TGLNDRQKVALKE
                                       329
                                                                                                    269 SLVGFEMDITHLDGHKVHISRDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPK 328
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                                                                                                                                                                                                               162 PVTCGRCHGAGVINVDTQTPLGMMRRQVTCDVCHGRGKEIKYPCTTCHGTGHEKQAHSVH 221
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                                                                                                                                          VKIPAGVETGQQIRLAGQGEAGFNGGPYGDLYVVVSVEASDKFEREGTTIFYNLNLNFVQ
                                                                                                                                                                            VEIEPGVRDGMEYPFIGEGEPHVDGEP-GDLRFRIKVVKHPIFERRGDDLYTNVTVSLVE 268
                                                                                                                                                                                                                                                                                QGDDLQYRVNLTFEEAIFGTEKEVKYH----REA-GCRTCN------GSGAKPGTS 161
                                                                                                                                                                                                                                                                                                                                                                                QYDTYGEEGLKDGHQSSHG------DIFSHFFGDFGFMFGGTPRQQDRNIPR 130
                                                                                                                                                                                                                                                                                                                                                                                                                             EFYDRLGVSKNASADEIKKAYRKLSKKYHPDIN-KEPGAEDKYKEVQEAYETLSDDQKRA 63
                                     EQLTEEAREGIKQ
                                                                     AALGDTVDIPTVHG-DVELVIPEGTQTGKKFRLRSKGAPSLRGGAV-GDQYVTVNVVTP-
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                                                                                                                                                                                                                                                                                                                                                        AYDQYGAAGANGGFGGAGGFGGFNGAGGFGGFEDIFSSFFGG-----GGSSR--NPNAPR 116
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 351
                                     341
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STREPTOCOCCUS PNEUMONIAE
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RESULT 11 US-08-868-288A-3

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                                                                                                                                                            RESULT
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                                              GENERAL INFORMATION:
APPLICANT: Au-Young
APPLICANT: Lal, Pro
APPLICANT: Bandman
                                                                                                            Sequence 3, Application Patent No. 6001598
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local S
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INFORMATION FOR SEQ ID NO: 3:
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NAME: Billings, Lucy J.
REGISTRATION UNMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: HNT2R
CLONE: 260873
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                               APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
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CORRESPONDENCE ADDRESS:
               NUMBER OF SEQUENCES:
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TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
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OPERATING SYSTEM:
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                                                                                                                           Application US/09235373
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                                                             Au-Young, Janice
Lal, Preeti
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US-09-388-993-3
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Best Local Similarity 46.2%;
Matches 60; Conservative 18
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                    APPLICANT: Au-Young, Janice
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MEDIUM TYPE: Diskette
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                            123 FGNRRGPRGS 132
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                                                     COUNTRY: UZIP: 94304
                                                                                                   STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 DFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDD-PQAQEKFQDLGAAYEVLSDSEKR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 DIYDKYGKEGLNGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDPFEDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 KQYDTYGEEGLK-DGHQSSH------GDIFSHFFG---DFGFMFGGTPRQQ- 125
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                                                                                        STATE:
                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
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                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNT2RAT01
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IBM Compatible
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, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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NAME:

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RESULT 14
US-08-868-288A-7
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; LIBRARY: HNT2RAT01
; CLONE: 260873
US-09-388-993-3
                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,288A
FILING DATE: June 3, 1997
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08868288A Patent No. 5922567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Laid, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 -- DRNIPRGS 132
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                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                      94304
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3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.6%; Score 257; DB 3; Length 330; 46.2%; Pred. No. 3.4e-20; ative 18; Mismatches 30; Indels
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RESULT 15
US-09-235-373-7
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Best Local Similarity
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                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/80
FILING DATE: June 3, 199;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
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ADDRESSE: Incyte Pharmaceuticals, Inc.
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APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
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                                                             LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM:
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STATE: CA
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CLONE: 32470
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Lal, Preet
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FastSEQ for Windows Version
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47.6%; Pred. No. 1.7e-17;
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LIBRARY: GenBank

CLOONE: 32470

US-09-235-373-7

Query Match

Best Local Similarity 47.5%; Pred: A1.76-17;

Matches 50; Conservative 14; Mismatches 22; Indels 19; Gaps 3;

Matches 50; Conservative 14; Mismatches 22; Indels 19; Gaps 3;

Matches 50; Conservative 14; Mismatches 22; Indels 19; Gaps 3;

Matches 50; Conservative 14; Mismatches 22; Indels 19; Gaps 3;

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Matches 50; Conservative 14; Mismatches 22; Indels 19; Gaps 3;

Matches 50; Conservative 14; Mismatches 19; Gaps 3;

Matches 50; Conservative 14;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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N. meningitidis st
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Homo sapiens fetal
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A human MCG18 prot
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DnaJ-related
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1 MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDD 1 MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDD 60

Query Match
Best Local Similarity
Matches 358; Conserv

99.8%; ilarity 100.0%; Conservative

Score 1879; DB 1; ;; Pred. No. 6.7e-184; 0; Mismatches 0;

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im 1; s representation in 1; continuous representation r	c_differecc_differecc_differecc_differecc_differecc_differecc_life	JT 1 W94065 standard; Protein; 358 W94065; W94065; W94065; Human DnaJ-like protein, HSPJ1 DnaJ-like protein; heat shock Immune disorder; inflammation;	85.5 85.5 85.5 85.5 85.5 85.5 85.5 85.5
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rig lA-D; 73pp; English. resents a human DnaJ-like proteins which id HSPJ2) and nucleic acid itaining a vector comprision of recombinant proteins and training a vector comprision of recombinant proteins and training a vector comprision of recombinant proteins and training a vector comprision and lymphoma; immune deficiency syndrom mellitus, multiple sclero, itic infections and inflit tissue damage, e.g. in it tissue damage, e.g. in and may be expressed from and may be expressed from a fill the nucleic acids are and quantifying the HSPJ and and/or amplification and/or ribozyme molecu 358 AA;	0 1 55 55 10	Protein; rst entry) protein, H n; heat sh inflammat	953 1 953 1 806 1 1482 1 589 1 764 1 394 1 1195 1 1195 1 1292 1 1456 1
Claim 1: Fig 1A-D; 73pp; English. This represents a human DnaJ-like protein, HSPJ1. The inventive human DnaJ-like proteins which are heat shock proteins (HSPJ1 and HSPJ2) and nucleic acid sequences encoding the pucells containing a vector comprising the nucleic acids are used to remain and lymphoma; immune disorders (typical of many dialeukaemia and lymphoma; immune disorders (typical of many dialeukaemia) and lymphoma; immune disorders (typical of many los many dialeukaemia) and lymphoma; immune disorders (typical of many los many dialeukaemia) and lymphoma; immune disorders (typical of many los many dialeukaemia) and lymphoma; immune disorders (typical of many los many dialeukaemia) and lymphoma; immune disorders (typical of many dialeu	ualifier: known coded by known coded by production coded by coded by production producti	יסי ⊳	R76707 R90923 R27481 R44193 P60303 W26727 W61252 R05530 R05530 R05530 R49042 R35221
ike protein, HSPJ1. hich are heat shock acid sequences enco rising the nucleic and secuentiant H and to screen for sp or prevent a wide v disorders (typical disorders (typical disorders rheumatoid inflammation. Agoni in cases of ankylo v, insulin dependent from a vector contar are used as primer HSPJ-encoding nucle tion assays, therap lecules, and for ch	AAN" TAN" aJ-like pr	ALIGNMENTS A. rotein; HSPJ1; tissue damage;	
re heat shock proteins aguences encoding the the nucleic acids are accombinant HSPJI and iscreen for specific biscreen for specific and years (typical of many callergy, asthma, Croha, rheumatoid arthritis, rheumatoid arthritis nation. Agonists may be so of ankylosing sponiation. Agonists may be seed as primers and project of as primers and project of as primers and project acid is coding nucleic acid is coding nucleic acid is says, therapeutically s, and for chromosome is	isorders	;; HSDJ2; can	
Fig lA-D; 73pp; English. Fig lA-D; 73pp; English. And HSPJ2 and nucleic acid sequences encoding the proteins. Host intaining a vector comprising the nucleic acids are used for the north proteins. Recombinant proteins. Recombinant proteins. Recombinant proteins are used for the north proteins. Recombinant proteins are used to treat or prevent a wide variety of solid cancers, and lymphoma; immune disorders (typical of many disclosed are immune deficiency syndrome, allergy, asthma, Crohn's disease, mellitus, multiple sclerosis, rheumatoid arthritis, microbial sitic infections) and inflammation. Agonists may be used to treat itschaemia, UV exposure, insulin-dependent diabetes and for wound and may be expressed from a vector containing the nucleic acids are used as primers and probes for y and quantifying the HSPJ-encoding nucleic acid in usual ation and/or amplification assays, therapeutically as antisense, forming or ribozyme molecules, and for chromosome mapping.	- for diagnosis,	; cancer; leukaemia; tes; wound healing;	Recombinant cold-r F. bidentis pyruva RP-III residual pr Rat NMDA receptor Sequence encoded b Yeast Mps1p protei Salicylic acid ind High density lipop High density lipop NMDA receptor chan Proctase B. Procta

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                                                                                                                                                                                                                                     Example 1; Fig 2A-B; 26pp; English.

This polypeptide sequence is encoded by the maize DnaJ-related gene (see T84330). DnaJ-related proteins assist in chaperone-mediated protein folding and provide cell viability at high temperatures. They are also involved in DNA replication, translation and peptide translocation across intracellular membranes. Due to this wide range of functions, DnaJ has a wide range of effectiveness and the gene's promoter sequence, ZmDJ1 (see T84329), is effective in a wide range of tissues. The claimed ZmDJ1 promoter can be used in claimed methods for control of antifungal or insecticidal genes in transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                         specific promoters, partic. insecticide genes
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tobacco DnaJ-related sequence, ZmDJ1 - is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DnaJ-related protein; chaperone; protein folding; DNA replication;
translation; peptide translocation; ZmDJ1; promoter; maize;
transgenic plant; insecticide; antifungal; fungicide;
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; T84330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbour E, Baszczynski C,
WPI; 97-145697/13.
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26-JUL-1995; US-001522.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crop protection.
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                                                       YDTYGEEGLKD--GHQSSH---GDIFSHFFG-DFGFMFGGTPRQQDRNIPRGSDIIVDLE
                                                                                             YYEILGVPKSASQDDLKKAYRKAAIKNHPDKGGD----PEKFKELAQAYEVLSDPEKREI 69
                                                                                                               FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ
                                        YDQYGEDALKEGMGGGGSHVDPFDIFSSFFGPSFG---GGGGSSRGRRQRRGEDVVHPLK 126
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35.8%;
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intermediate between constitutive and tissue
partic. for control of antifungal and
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-ARQAPGKRKCNCRQEMRTTQLGPGRF 185
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.1e-44;
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                                                                                                                                                                                   Length 419;
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YDQYGEDALKEGMGGGGSHVDPFDIFSSFFGPSFG--

-GGGGSSRGRRQRRGEDVVHPLK

Query Match Best Local Matches

Similarity

27.3%;

Conservative

61;

Score 515; DB 1; Pred. No. 2.1e-44; 1; Mismatches 115

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Length 419 Indels

FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ

YYEILGVPKSASQDDLKKAYRKAAIKNHPDKGGD-

-PEKFKELAQAYEVLSDPEKREI

69 85

YDTYGEEGLKD--GHQSSH---GDIFSHFFG-DFGFMFGGTPRQQDRNIPRGSDIIVDLE

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Maize ZMDJI promoter - and corresponding recombinant expression
PT systems and transgenic plants
PS Example 1; Fig 2; 16pp; English.

C The present invention describes the maize ZMDJI control sequence. Also
C EMDJI control sequence linked to a heterologous protein coding sequence;
C ZMDJI control sequence linked to a heterologous protein coding sequence;
C ZMDJI control sequence which retain transcription-initiating activity and/or
C contain the expression system; (3) DNA comprising fragments of the ZMDJI
C control sequence which retain transcription-initiating activity and/or
C the function of the leader sequence; and (4) a method to regulate the
C expression of a gene under control of the ZMDJI control sequence in
C comprising modifying the cell, parts, where the plant is a monocotyledon,
C control of the ZMDJI control sequence to contain the DNA of (3) or RNA
C of the same nucleotide sequence. Expression systems as described above
C in which the heterologous sequence in insecticidal or antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
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protein can be used to produce transgenic maize plants resistant to insects (e.g. European corn borer) or fungi (e.g. Ostrinia nubilalis). The control sequence comprises a constitutive promoter that directs transgene expression in various plant tissues, including 11-week-old leaf blades, leaf whorls, leaf collars, stalk rind, stalk pith, stalk nodes, roots and kernels. The present sequence represents the protein sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W83397
W83397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
Barbout E, Baszczynski C, Horow:
WPI, 99-059853/06.
N-PSDB; V72905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize DnaJ clone protein sequence.
Maize; Zea mays; transcriptional promoter; control sequence; ZMDJI;
DnaJ clone; corn; insecticide; antifungal protein; transgenic plant;
insect resistance; European corn borer; fungal resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUL-1995; US-001552
26-JUL-1996; US-686417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5850018-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ostrinia nubilalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 DPGEVVKPDQFKAINDEGMPIYQRPFMKGKLYIHFTVEFPDSLAPEQCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D--KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAPDTVTGDIVFVLQQKDHSKFKRKGEDLFYEHTLSLTEALCGFQFVLTHLDNRQLLIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQMQQ-PCNECKGTGESINEKDRCPGCKGEKVIQEKKVLEVHVEKGMQHNQKITFPGEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSLEDLYNGTSKKLSLSRNVICSKCKGKGSKSGASMRCPGCQGSGMKVTIR--QLGPSMI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horowitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosichan JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303
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 밁
                                                                                                                                                                                                                                                     For the diagnosis, monitoring or treatment of cancers

PS Disclosure; Page 456-457; 787pp; English.

CC The invention relates to a method for diagnosing a disorder characterised

CC by expression of a human cancer associated antigen precursor coded for by

CC biological sample isolated from a subject with an agent that specifically

CC binds to the NAM, an expression product or a fragment of an expression

CC product complexed with an HLA molecule; and (b) determining the

CC interaction between the agent and the NAM or the expression product as a

CC determination of the disorder. The products and methods can be used in

CC the diagnosis, monitoring, research, or treatment of conditions

CC characterised by the expression of various cancer associated antigens.

CC The invention provides nucleic acid sequences and encoded polypeptides

CC which are cancer associated antigen precursors expressed in human breast

CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998; U14679; 22-JUL-1998; US-102322. 22-JUN-1998; US-102322. 17-JUL-1997; US-986164. 10-OCT-1997; US-061765. 10-OCT-1997; US-081765. 11-OCT-1997; US-081765. 11-OCT-1997; US-0817697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES.
Chen Y, Gout I, Gure A, OHare M, Obata Y, Old
Pfreundschuh M, Sahin U, Scanlan MJ, Stockert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tureci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9904265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breast cancer; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Renal cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y07061 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D--KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAR
                                                                                      AVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQE-KFQDLGAAYEVL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99-132448/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAPDTVTGDIVFVLQQKDHSKFKRKGEDLFYEHTLSLTEALCGFQFVLTHLDNRQLLIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQMQQ-PCNECKGTGESINEKDRCPGCKGEKVIQEKKVLEVHVEKGMQHNQKITFPGEAD
SNPEKRELYDRYGEQGLREGSGGGGWHGLIFSLTVFCGGLFGFM--GNQSRSRNGRRRGE 116
                     SDSEKRKQYDTYGEEGLKDGHQSS--HGDIFS---HFFGDFGFMFGGTPRQQDRNIPRGS 132
                                                                    ANVADTKLYDILGVPAGASENELKKAYRKLAKEYHPDKN---PQMQETNFKEISFAYEVL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QMTQEVVCDECPNV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSLEDLYNGTSKKLSLSRNVICSKCKGKGSKSGASMRCPGCQGSGMKVTIR--QLGPSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLEEVYAGNFVEVVRNKPV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer associated antigen precursor sequence.
associated antigen; diagnosis; research; treatment; human;
                                                                                                                                                          Similarity
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                        27.1%; *Score 509.5; DB 1 37.0%; Pred. No. 7.6e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415
                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KLVNEERTLEVEIEPGVRDGMEXPFIGEGE
                                                                                                                                                                        DB 1;
                                                                                                                                        122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n Ľ
                                                                                                                                                                     Length
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      develop products
                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung
                                                                                                                                    Gaps
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24 24 25 25

131 117

QGDDLQYRVNLTFEEAIFGTEKEVKYH----

-GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQ 189

-REA-GCRTCN-

GSGAKPGTS

161

64

AYDQYGAAGANGGFGGAGGFGGFNGAGGFGGFEDIFSSFFGG

QYDTYGEEGLKDGHQSSHG-----

----DIFSHFFGDFGFMFGGTPRQQDRNIPR 130

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                                                                                                                                                                         PT Streptococcal heat shock proteins and corresponding DNA sequences - PT used in the production of a vaccine to treating and preventing strain-specific Streptococcal infection
PS Example 3; Page 93-94; 156pp; English.

CC This amino acid sequence corresponds to the N-terminal portion of the Streptococcus pneumoniae DnaJ protein. The protein shows a high degree CC of identity (72% and 51%) to the DnaJ proteins from Lactococcus lactis and E. coli respectively. The sequence encoding this truncated protein CC was isolated on the same nucleotide sequence that encodes the CC s. pneumoniae heat shock protein 72 (HSP72; W22357). The nucleotide fragment was isolated from a HindiII-partially digested genomic DNA CI intrary using a fragment of the chimaeric gene (T73392) corresponding to the sequence encoding the C-terminal 169 amino acids of HSP72. The HSP72 CC protein and its fragment, or antibodies specific to HSP72, are used in CC pharmaceutical compositions, pref. a vaccine, for treating or preventing CC infection by S. pneumoniae or related bacteria in humans, e.g. Cc. S. pyogenes or S. agalactiae.
                                                                        Matches
                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995; CA0322.
07-JUN-1995; US-472534.
04-AUG-1995; US-001805.
(IAFB-) IAF BIOVAC INC.
Brodeur B, Hamel T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. pneumoniae N-terminal portion of DnaJ protein.
Streptococcus pneumoniae; S. pyogenes; S. agalactiae; genome; HSP open reading frame; heat shock protein 72; DnaJ; DnaK; chimaeric; E. coli; Lactococcus lactis; antibody; vaccine; infection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae.
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T73388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09640928-A1.
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                    DFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHIS--RDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEGEPHVDGEPGDLRFRIKVVKH-PIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGMVQQMQSVCSDCNGEGEVINEKDRCKKCEGKKVIKEVKILEVHVDKGMKHGQRITFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMMHPLKVSLEDLYNGKTTKLQLSKNVLCSACSGQGGKSGAVQKCSACRGRGVRIMIRQL
EFYDRLGVSKNASADEIKKAYRKLSKKYHPDIN-KEPGAEDKYKEVQEAYETLSDDQKRA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97-052328/05.
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                                                                                         Similarity
                                                                                                                                                                352 AA;
                                                                    18.3%;
llarity 28.4%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352
                                                                        55;
                                                                    Score 345; DB 1;
Pred. No. 3.9e-27;
5; Mismatches 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rioux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
                                                                                                        Length 352;
                                                                        Indels
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                                                                        82;
                                                                      Gaps
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W98475
ID W98475
AC W98475
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08-OCT-1998.
01-APR-1998; U06371.
29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases claim 8; page 853-855; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, a peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used sequence and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb
MPI; 98-542293/46.
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GHPO protein; Helicobacter
peptic ulcer disease.
Helicobacter pylori.
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10-DEC-1998; U11182.
02-JUN-1997; US-868288.
03-JUN-1997; US-868288.
(INCY-) INCYTE PHARM INC
This represents a human DnaJ-like protein, HSPJ2. The invention provides two human DnaJ-like proteins which are heat shock proteins J1 and J2 (HSPJ1 and HSPJ2) and nucleic acid sequences encoding the proteins. Host cells containing a vector comprising the nucleic acids are used for the production of recombinant proteins. Recombinant HSPJ1 and HSPJ2 are used to raise Ab, therapeutically and to screen for specific binding agents. Antagonists are used to treat or prevent a wide variety of solid cancers, leukaenia and lymphoma; immune disorders (typical of many disclosed are acquired immune deficiency syndrome, allergy, asthma, Crohn's disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, microbial and parasitic infections) and inflammation. Agonists may be used to treat or prevent tissue damage, e.g. in cases of ankylosing spondylitis, heart attack, ischaemia, UV exposure, insulin-dependent diabetes and for wound
                                                                                                                                                                                                                                                                                                                Claim 22; Fig 3A-D; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding human DnaJ-like proteins - for treatment and prevention of cancer, immune disorders and
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DnaJ-like protein; heat shock protein; HSPJ1; HSPJ2; cancer; limmune disorder; inflammation; tissue damage; diabetes; wound
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Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                potential vaccines

Claim 13; Pages 56-57; 76pp; English.

Claim 13; Pages 56-57; 76pp; English.

The sequence is that of a secreted protein from a human fetal

Ridney clone AK296. Such a sequence is predicted to have biological

activities which would make them suitable for treating, preventing of

ameliorating medical conditions in humans and animals, although no

supporting data is given. Suggested activities include nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             healing, and may be expressed from a vector containing the nucleic acids. Fragments of the nucleic acids are used as primers and probes for detecting and quantifying the HSPJ-encoding nucleic acid in usual hybridisation and/or amplification assays, therapeutically as antisense, triplex-forming or ribozyme molecules, and for chromosome mapping
                                                                                                                                                                                                                            and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene
                                                                                                                                                                                                                                                                       activity cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, haemostripin/inhibin activity, chemotactic/chemokinetic activity, haemos
                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding secreted human proteins - from foetal kidney or adult retina cDNA libraries, use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merberg D, Racie L
WPI; 99-095671/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-1998; U13530.
30-JUN-1997; US-885610.
(GEMY) GENETICS INST 1
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Merberg D, Racie LA, Treacy
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sapiens fetal kidney clone
eted protein; fetal kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDD-PQAQEKFQDLGAAYEVLSDSEKR
                                                                                        PQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQ
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AEAKFREIAEAYETLSDANRRKEYDTLGHSAFTSGKGQRGSGSSFEQSFNFNFDDLFKDF
                              AQEKFQDLGAAYEVLSDSEKRKQYDTYGEEGLKDG------HQSSHGDIFSHFFGDF
                                                            PQSIFIFAICILMITELILASKSYYDILGVPKSASERQIKKAFHKLAMKYHPDKN-KSPD
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Pred. No. 3.5e
18; Mismatches
                                                                                                                   Score 254; DB
Pred. No. 4e-1
33; Mismatches
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Best Local
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01-APR-1998; U06371.

29-JUL-1997; US-902615.

01-APR-1997; US-833457.

24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 8; Page 773-774; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, a peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also used for the production of antibodies. The products can also be used detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHPO protein; Helicobacter infection; gastroduodenal disease; peptic ulcer disease. Helicobacter pylori. W09843478-Al.
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(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
(INMR) MERIEUX ORAVAX H. Miller C, Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; X14165
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                                                     EGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQ 345
                                                                                                                                                  RDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKR
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KGIKNRKTSHV-GDLYLQARLILPK---TETLSNELKALLEK
                                                                                                                                                                                                                                                                                      MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHVDGEP--GDLRFRIK 244
                                                                                                                                                                                                                                                                                                                                            FAPENLDITAALNVSVLDTLLGNKKQVSIN------
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26.0%;
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Pred. No. 9.7e-17;
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RESULT Y11105 ID Y1 AC Y1

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Y11105; Y11105;

standard;

Protein;

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RESULT
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Best Local S
Matches 82
    H. pylori ORF 05cel0910_23712780_cl_4 cytoplasmic prote Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein; cytoplasmic protein; cellular protein Helicobacter pylori.
WO9824475-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. pylori and other Helicobacter species
Claims 37, 41; Bage 271-272; 339pp; English.
Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 97 ORFs are shown. The proteins are variously cell envelope proteins, cytoplasmic proteins, secreted proteins or other cellular proteins.
Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                  Yll104 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9824475-A1.
11-JUN-1998.
05-DEC-1997; U
14-JUL-1997; U
05-DEC-1996; U
25-MAR-1997; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Helicobacter pylori nucleic products for the diagnosis, prevention ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASTR ) ASTRA AB.
Alm RA, Castriotta LM,
WPI; 98-333051/29.
N-PSDB; X30634.
                                                                                                                                                                                                  251
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H. pylori OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -JUN-1999 (first entry)
pylori ORF hp7e10192_23712780_f2_5 cytoplasmic protein.
ccine; probe; diagnostic; ORF; cell envelope protein;
creted protein; cytoplasmic protein; cellular protein.
                                                                                                                                                                                              IKSRKTSHVGDCIASSFDL--PK
                                                                                                                                                                                                                          LPNFDNNNIKGSLITTFDVDFPK
                                                                                                                                                                                                                                                                              KHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHK-VHISRDKITRPGAXXWKKGEG
                                                                                                                                                                                                                                                       EDEMYRREKDDIIQIFDLPLKTALFGGKIEIA--TWHKTLTLTIPPNTKAMQKFRIKDKG
                                                                                                                                                                                                                                                                                                                                              MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHVDGEPGDLRFRIKVV
                                                                                                                                                                                                                                                                                                                                                                                                       NIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     RQYDQFGDNMFGGQNFSDFARSRGPSEDLDDILSSIFGKGGFSQRFSQNSQGFSGFNFSN
                                                                                                                                                                                                                                                                                                                                                                            FAPENLDVTAILNVSVLDTLLGNKKQV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQYDTYGE----EGLKD-----GHQSSHGDIFSHFFGDFGFMFGGTPRQQ------DR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSLYQTLNVSENASQDEIKKSYRRLARQYHPDLN-KTKEAEEKFKEINAAYEILSDEEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 25.4
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-891928.
US-759625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-823745
                                                                                                                                                                                                                                                                                                                 -----SVNNE-TFSLKIPIGVEEGEKIRVRNKGKMGRTGR-GDLLLQIHIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%;
25.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 239;
Pred. No. 1
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
.9e-16;
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RESGUA
R90600
ID R9
AC R9
DT 07
DE MC
KW DC
KW DC
KW OOI
OS MC
KW OOI
OS MC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PT New isolated Helicobacter pylori nucleic acids - used to develop PT products for the diagnosis, prevention and treatment of infection by PT H. pylori and other Helicobacter species PS Claims 37, 41; Page 270-271; 339pp; English.

CC Recombinant or substantially pure preparations of H. pylori polypeptides CC are disclosed, together with the nucleic acids encoding them. In all, CC 97 ORFs are shown. The proteins are variously cell envelope proteins, CC vaccines containing the nucleic acids or proteins are claimed, as are CC vaccines containing the nucleic acids or proteins are claimed, as are CC robes containing at least 8 nucleotides from the nucleic acid CC sequences. The vaccines are useful for treating or reducing the risk of CC detecting the presence of Helicobacter in a sample. The products are CC used used to screening for compounds having the ability to interfere CC with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                       Mouse; Cysteine string protein; anergy; T-lymphocyte; differential display; cDNA; reverse transcription; probe polymerase chain reaction; cloning; gel electrophoresis; antibody; diagnostic; immunoassay; autoimmune disease;
04-JAN-1996.
22-JUN-1995;
                             WO9600300-A1.
                                                                                      misc_difference
                                                                                                                    misc_difference
                                                                                                                                                                                                                                                      R90680;
07-APR-1996
                                                          misc_difference
                                                                                                                                                               organ
                                                                                                                                                                                                                                     Mouse cysteine string protein
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14-JUL-1997;
05-DEC-1996;
25-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 RDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKR 83
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                                                                                                                                                                                                                                                                                                                                                         EDEMYRREKDDIIQIFDLPLKTALFGGKIEI
                                                                                                                                                                                                                                                                                                                                                                                     KHPIFERRGDDLYTNVTVSLVESLVGFEMDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAPENLDVTAILNVSVLDTLLGNKKQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQYDQFGDNMFGGQNFSDFARSRGPSEDLDDILSSIFGKGGFSQRFSQNSQGFSGFNFSN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQYDTYGE-----EGLKD-----GHQSSHGDIFSHFFGDFGFMFGGTPRQQ-----DR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSLYQTLNVSENASQDEIKKSYRRLARQYHPDLN-KTKEAEEKFKEINAAYEILSDEEKR 61
                                                                                                                                                             transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98-333051/29.
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                                                                                                                                                                                                                                                    (first entry)
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US-891928.
US-759625.
US-823745.
                                                            191
                                                                                         183
                                                                                                                     168
                                                                                                                                Location/Qualifiers
                                            /note-
                                                                        /note=
                                                                                                      /note=
                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                SVNNE-TFSLKIPIGVEEGEKIRVRNKGKMGRTGR-GDLLLQIHIE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%;
26.9%;
                                                                                                                                                             vaccine;
                                                                       "In-frame
                                                                                                   "In-frame
                                           "In-frame
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Pred.
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                                                                                                                                                             drug
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                                         stop codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 2.
                                                                                                                                                             screening
                                                                     codon"
                                                                                                    codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 1;
2.1e-16;
hes 92;
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                                                                                                                                                                                                         probe;
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Query Match
Best Local
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The sequence represents a mouse cysteine string protein encoded by a gene isolated from mouse T-cell clones 11.3.7 and 12.2 by a new procedure for identification of genes associated with anergy. The protein is expressed in resting T-cells but not in anergic T-cells To isolate proteins of this type, differential display is first performed by generating cDNA from polyA+ mRNA with an oligo-dT primer with 2 variable anchor nucleotides at the 3'-end, e.g.

Thir86, using reverse-transcriptase. The resulting cDNA promise in the communication of the content o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       populations are amplified by the polymerase chain reaction, using the same oligo-dr primer and a 5'-primer which includes using the same oligo-dr primer and a 5'-primer which includes common 4-5 nucleotide sequence combinations, e.g. T11785. After gel electrophoresis of the products, bands unique to anergised gel electrophoresis of the products, bands unique to anergised non-anergised cells are excised, eluted, amplified, cloned and sequenced. Genes and proteins (and corresponding antibodies) arising from this procedure may be used e.g. in monitoring
                                                                                                                                                                                                                                                                           Misc_difference
                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein AM610.
Human; secreted protein; ATCC 98026;
cell proliferation; differentiation;
                                  Misc_difference
                                                                                 Misc_difference
                                                                                                                               Misc_difference
                                                                                                                                                                            Misc_difference
                                                                                                                                                                                                                            Misc_difference
                                                                                                                                                                                                                                                                                                                         Misc_difference
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      W44076 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             effectiveness, and in drug screening. Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR. Bloom D, Fathman G; WPI; 96-068884/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                         W44076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSE 81: | | | :||: :: |: :|:|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRNIYDKYGSLGLYVAEQFGEENVNTYF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRKQYDTYGEEGLKDGHQSSHGDIFSHF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGESLYHVLGLDKNATSDDIKKSYRKLALKYHPDKNPDNPEAADKFKEINNAHAILTDAT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 38; Conserv
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                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                            /note=
96
                                                                               /note=
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 82
/label= Unspecified
/note= "encoded by TGA a stop codon"
                                              /note=
                                                                  /label=
                                                                                                               /label=
                                                                                                                                                            /label= Unspecified
                                                                                                                                                                                             /note=
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43.2%;
                                                                                             "encoded by "
                                                                                                                                             "encoded by
                                                                                                                                                                                        "encoded by TAG
                                                                                                                                                                                                                                          "encoded by TGA a stop codon"
                                                "encoded
                                                                                                                                                                                                                                                                                       "encoded by AGN"
                                              Unspecified 
"encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                         159
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Pred. No. 3e-14;
23; Mismatches
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                                                                                                                                              RGR"
                                                 RAG"
                                                                                                                                                                                                                                                                                                                                                                        regulation.
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18-APR-1996; US-634325.
(GEMY) GENETICS INST INC
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The partial CDNA clone AP162 was 1st isolated from a human adult placenta cDNA clone AP162 was 1st isolated from a human adult placenta cDNA library. The partial cDNA clones AM931, AM610, AM340, AM282, AK647, AK533 and AK296 were 1st isolated from a human feetal kidney cDNA library. The partial cDNA clones H617 and BB9 were 1st isolated from a human peripheral blood monocyte cell (Th1 cor Th2) cDNA library. The partial cDNA clone AM191 was 1st isolated from a human ovary (PA-1 teratocarcinoma) cDNA library. The partial cDNA clones AT211, AT205 and AT319 were 1st isolated from a human clones AT211, AT205 and AT319 were 1st isolated from a human clones AS34 and AS32 were 1st isolated from a human foetal brain cDNA library. The partial cDNA clones AS34 and AS32 were 1st isolated from a human foetal brain cDNA library. The partial cDNA clone AR260 was 1st isolated from a human adult retina cDNA library. The partial cDNA clones K640 and K39 call tretina cDNA library. The partial cDNA clones K640 and K39 call tretina cDNA library. The partial cDNA clones K640 and K39 call tretina cDNA library. The partial cDNA clones K640 and K39 call tretina cDNA library. The partial cDNA clones K640 and K39 call tretina cDNA library. The partial cDNA clones K640 and K39 call tretina cDNA library.
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The present sequence is a human secreted protein, which may have nutritional uses, or cytokine and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haematopoiesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, anti-inflammatory or tumour inhibition activities
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12-APR-1996; US-631184.
(MURO-) MURO PHARM INC.
Theoharides TC;
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                                                                                                                                                                                                                                                                                                                   which is a putative serine protease. TI genes function in biochemical pathways involved in weight control and related disorders. The products can be used for treating weight disorders, e.g. obesity, cachexia or anorexia nervosa, or a related disorder such as diabetes. The products can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus Tub Interactor (mTI-3) protein.
serine protease; tub interactor; treatment; obesity; cachexia;
anorexia nervosa; diabetes; cell cycle progression; apoptosis;
neurodegenerative disease; Alzheimer's disease; drug screening;
parkinson's disease; Huntington's chorea; detection; diagnosis;
amylotrophic lateral sclerosis; spinocerebellar degeneration.
                                                                                                                                                                                                                                                                                                                                                                                             Claim 28; Fig 4; 120pp; English. The sequence is that encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tub interactor genes of obesity, cachexia,
                                                                                                                                                                                                                           which are characterised by apoptosis, including Alzheimer's disease, Parkinson's disease, Huntington's chorea, amylotrophic lateral sclerosis or spinocerebellar degenerations. The products can also be used for detection, diagnosis and
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05-SEP-1997;
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W59132;
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                                                                          RDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPD-----DPQAQEKFQDLGAAYEVLS 78
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; LIBRARY: SYNO; ; CLONE: 136466 US-09-235-373-2
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Patent No. 6001598
                                                                                                                                                                            APPLICATION NUMBER: 08/868,28
FILING DATE: June 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                     STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
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MEDIDIM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FasteEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE
NUMBER OF SEQUENCES: 7
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TYPE: n
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STATE: CA
COUNTRY: USA
ZIP: 94304
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415-845-4166
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; IMMEDIATE SOURCE:
; LIBRARY: SYNORA
; CLONE: 136466
US-09-388-993-2
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Matches 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1376 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/868,28
EILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                       Local Similarity
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TCTCACCGGGACTCGGGACTCCCGGGAAGTGGACCGGCAGAAGAGGGGGCTAGCTTG
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                                          Conservative
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                                                                                                                                                                                 single
                                                      99.9%; Score 1374;
100.0%; Pred. No. 0;
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 GGAGCGAANTANTGGAAGAAAGGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAG
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US-08-868-288A-4
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                                                                                     Query Match
Best Local Similarity
Matches 147; Conserv
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                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFHAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                               TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 POIL
STREET: Palo Alto
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: (FILING DATE: June 3, PRIOR APPLICATION DATA: APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
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APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
       328
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CLONE: 260873
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                                          GATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCC 327
TATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTG---ATGATCCACAAGCC
                           GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAAGGCA
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                                                                                  Score 91.4; DB 4;
Pred. No. 3.8e-17;
0; Mismatches 71;
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US-09-235-373-4
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                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/868,288
FILING DATE: June 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J. 749
REGISTRATION NUMBER: 95.749
REFERENCE/DOCKET NUMBER: PF-0309
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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CITY: Palo Alto
CTATE: CA
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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385 CAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGG 444
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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for Windows Version
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                                                                                                                                                                         Score 91.4; DB 5;
Pred. No. 3.8e-17;
0; Mismatches 71;
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                                                                                                                                                                                                       Length 1330;
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US-09-388-993-4
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Best Local Similarity
Matches 147; Conserv
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Patent No. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: line
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APPLICATION NUMBER:
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                                                                                                                                                    328 TATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTG---ATGATCCACAAGCC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 AAACAGTACGATACTTATGGTGAAGAAGGATTAAAAGATGG
 343 GACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTGG
                                445 AAACAGTACGATACTTATGGTGAAGAAGGATTAAAAGATGG 485
                                                                                   385 CAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGG
                                                                                                                                 223
                                                                                                                                                                                                 163 GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAAGGCA 222
                                                                                                                                                                                                                    268 GATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCC
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OPERATING SYSTEM: DOS
COFTWARE: FASTSEQ FOR Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 GAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                             LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                GAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGG
                                                                                                                                 TATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAAGAAGAAGCA
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3174 Porter Drive
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Best Local Similarity 56.3%;
Matches 143; Conservative
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
342
                           502 GGAGACATTTTTC 515
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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                                                                           CGGAAACAGTACGATACTTATGGTGAAGAAGGATTAAAAGATGGTCATCAGAGCTCCCAT 501
                                                                                                              GCTGAGGAGAAGTTTAAGGAGATTGCAGAGGCCTATGATGTGCTAAGTGACCCCAAGAAA
                                                                                                                                  GCCCAGGAGAATTCCAGGATCTGGGTGCTGTTATGAGGTTCTGTCAGATAGTGAGAAA 441
                                                                                                                                                                        AAAGCCTACCGGAAGATGGCCTTGAAGTACCACCCAGACAAGAA---TAAAGAACCCAAC
                                                                                                                                                                                                     AAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGATCCACAA 381
                                                                                                                                                                                                                                    GGAAAAGATTATTACAAGATTCTTGGGATCCCATCGGGGGCCAACGAGGATGAGATCAAG 164
                                                     CGGGGCCTGTATGACCAGTATGGGGAAGGAAGGCCTGAAGACCGGCGGTGGCACATCAGGT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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Shah, Purvi
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Pred. No. 2.6e-09;
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US-08-486-955A-6
Sequence 14, Appli
Patent No. 5670367
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Best Local Similarity
Matches 119; Conserv
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 2001:
REFERENCE/DOCKET NUMBER: ?
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LENGTH: 672 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                       151
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ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
                                                                                                211 ACGAAAAGAAACATTTATGACAAGTATGG
                                                                                                                                436 GAGAAACGGAAACAGTACGATACTTATGG 464
                                                                                                                                                                                             376 CCACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGT 435
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                                                                                                                                                                                                                                                                                                                                   256 ATTGCCGGACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGAT 315
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Four Milward CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                ATTAAAAAGTCCTATCGGAAGCTGGCCCTGAAGTATCACCCTGACAAGAACCCTGATAAC 150
                                                                                                                                                                                                                                                        ATTAAAAAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGAT 375
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                Application US/08232463
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Pred. No. 1.3e
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Suite 3400
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GENERAL INFORMATION:
APPLICANT: DORNER,
APPLICANT: SCHEIFI
APPLICANT: FALKNEI

DORNER, F.

SCHEIFLINGER, FALKNER, F. G.

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US-08-232-463-14
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Best Local
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                             1210
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
1090 RRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCGGAA 1031
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APPLICATION NUMBER: 1
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NUMBER OF SEQUENCES:
                                                                                                                                                                                              704
                                                                                                                                                                                                                                                                                                                                                             524 TTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCCTCGTCAGCAAGACAGAAATATTCCAA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                          CTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAA 943
                                                                               TAGAAATAGAGCCTGGGGTGAGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGC 883
                                                                                                                                                                 GAGGAAGTGATATTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATT 643
                                                                                                                                                                                                                                                                                                                                    ATTGTCGGCAAGAGATGCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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52
                                                                                                                                                                                                                                                                                                                                                                                                                    4.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 59.4; DB 1
Pred. No. 2.6e-07;
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US-08-221-816B-1
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                    1235
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TELECOMMUNICATION INFORMATION:
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SOFTWARE: FastSEQ Version
CURRENT APPLICATION DATA:
                                                                                                                                                                    1175 GACGAGATTATTACAAAATCTTGGGAGTAAAAAAGAAATGCCAAAAAGCAAGAAATCATTA 1234
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
TITLE OF INVENTION: OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1030 TTAATTCTGTGAGCGTA 1014
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                                                                                                                                      323
   434 GTGAGAAACGGAAACAGTACGAT 456
                                                                                                                                                                                                      263 GACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAA 322
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-90
TELEFAX: (212) 869-8864
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                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                      -----AAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATA 433
                                                                                                    AAGCATACCGAAAATTAGCACTGCAGTGGCACCCAGACAACTTCCAGAACGAAGAAGAAA 1294
                                                                                                                                    AGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGATCCAC---
                                   AGAAAAAAGCTGAGAAGAAGTTCATTGACATAGCAGCTGCTAAAGAAGTCCTCTCCGATC 1354
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10036/2711
                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                            1515 base pairs
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Mathews, Michael B.
Katze, Michael G.
                                                                                                                                                                                                                                       3.9%;
ilarity 58.1%;
Conservative
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                                                                                                                                                                                                                                       Score 53.4; DB 2;
Pred. No. 5.6e-06;
0; Mismatches 76;
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1355 CAGAAATGAGGAAGAAGTTTGAT 1377

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                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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1410 AGAAAAAAGCTGAGAAGAAGTTCATTGACATAGCAGCTGCTAAAGAAGTCCTCTCCGATC 1469
                                                                         1350
                                                                                                                                         1290
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 204/139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 08/141,244
2011091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS (Version 5.0)
SOFTMARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/953,681
FILING DATE: September 29, 1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                        323
                                                                                                                                                    263 GACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAA 322
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MENTIN TYPE: 3.5" Diskette, 1.44 Mb
                                         380
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NUMBER OF SEQUENCES:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Douglas E. Olson
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
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                                                                                   AGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGATCCAC--- 380
                                                                                                                               GACGAGATTATTACAAAATCTTGGGAGTAAAAAGAAATGCCAAAAAGCAAGAAATCATTA 1349
                               -----AAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGATGAGGTTCTGTCAGATA 433
                                                              AAGCATACCGAAAATTAGCACTGCAGTGGCACCCAGACAACTTCCAGAACGAAGAAGAAA 1409
                                                                                                                                                                                                          118;
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Katze, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koromilas, Antonis E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         October 25, 1993
                                                                                                                                                                                                                                                                                                                                                       cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                                                                                      3.9%;
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Pred. No. 6e-06;
0; Mismatches 76;
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                                                                                                                                                             RESULT
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                                                                                                          Sequence 4, Application US/08472534 Patent No. 5919620
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Best Local Similarity
                                                                    GENERAL INFORMATION:
APPLICANT: Hamel, Josee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
     APPLICANT: Brodeur, Bern:
APPLICANT: Martin, Denis
TITLE OF INVENTION: HEAT
TITLE OF INVENTION: STREE
                                                                                                                                                                                                        1051 TTACCGGAAACGGGCCTTGATGCACCATCCAGATCGGCACAGTG 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       327 CTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTG 370
                                                                                                                                                                                                                                                                                    991
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                           AGATTACTACAAGATCCTGGGAGTGGACAAGAATGCCTCTGAGGACGAGATCAAGAAAGC 1050
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28 State Street
                                                                                                                                                                                                                                                                                                                                                  3.5%;
ilarity 66.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : (617)227-7400
(617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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HEAT SHOCK PROTEIN HSP72
STREPTOCOCCUS PNEUMONIAE
                                                      Bernard R
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>-1996
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                                                                                                                                                                                                                                                                                                                                                Score 48; DB 4; Length 1700, Pred. No. 0.00023; 0; Mismatches 35; Indels
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NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

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; LOCATION:
US-08-472-534-4
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.: 4320 base pairs

IYPE: nucleic acid

STRANDEDNESS: don'

TOPOLOGY: 1:
OLECULE
                                                                                                                             3337
                                                              3394
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
3454
                                                                                                                                                                                          3277 GAATTTTATGATCGTCTGGGGGGTATCCAAAAACGCTTCGGCAGACGAAATCAAAAAGGCT 3336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULL
HYPOTHETICAL: N
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-596-9000
                                                                                             388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: L- York
                              448 CAGTACGATACTTATGGTGAAGAAGGATTAAAAGATGGT 486
                                                                                                                                                            328 TATAGGAAACTAGCCCTGCAGCTTCATCCCGGACCGGAACCCTGATGATCCACAAGCCCAG 387
                                                                                                                                                                                                              268 GATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAAGGATATTAAAAAGGCC 327
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 682..2502
OTHER INFORMATION:
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OTHER INFORMATION: //
OTHER INFORMATION: DI
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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GCCTATGACCAGTATGGTGCTGCAGGCGCCAATGGTGGT 3492
                                                                                           GAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGGAAA 447
                                                                                                                             TATCGTAAGCTTTCCAAAAAATATCACCCAGATATCAAC---AAGGAGCCTGGTGCTGAG
                                                             GACAAGTACAAGGAAGTTCAAGAAGCCTATGAGACTTTGAGTGACGACCAAAAACGTGCT 3453
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                                                                                                                                                                                                                                                                        3.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Heat-Shock Protein 72"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "NH2-terminal portion of DNA J"
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                                                                                                                                                                                                                                                         Score 47.8; DB 4;
Pred. No. 0.00048;
0; Mismatches 97;
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                                                                                                                                                                               US-07-642-734C-3
                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us-08-879-260-3
                                                                                                                                           Sequence 3, Application US/07642734C Patent No. 5824513
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08879260 Patent No. 5935851
                                                                                                                               GENERAL INFORMATION:
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                             APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Recomb
TITLE OF INVENTION: Erythr
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, CURRENT APPLICATION DATA APPLICATION NUMBER: US/08/879,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                               1196 TTATCGGAAACGGGCCTTGATGCACCATCCAGATCGGCATAGTG 1239
                                                                                                                                                                                                                                                                                                               1136 AGATTACTACAAGATTCTAGGAGTGGACAAGAATGCCTCTGAGGACGAGATCAAGAAAGC 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                              327 CTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTG 370
                                                                                                                                                                                                                                                                                                                                     267 AGAITTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAAGGATATTAAAAAAGGC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: bot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1756 base pairs
                                                                                                               Katz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Edward H. Gorman
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                                                                                                                                                                                                                                                                                                                                                                                               3.3%;
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                                Erythromycin
27
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                                                             Recombinant DNA Method for Producing
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                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 19..4470
OTHER INFORMATION: /funct
OTHER INFORMATION: module
FEATURE:
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LOCATION: 97.1482
OTHER INFORMATION: /func
OTHER INFORMATION: beta
FEATURE:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SACCH
 FEATURE:
NAME/KEY:
                                                                                                        NAME/KEY: misc_feature
LOCATION: 4171..428
OTHER INFORMATION: /function= "OTHER INFORMATION: acyl carrier
FEATURE:
                                NAME/KEY: misc_feat
LOCATION: 4471..107
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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LOCATION: 19.10722
OTHER INFORMATION: /C
OTHER INFORMATION: /E
OTHER INFORMATION: /F
OTHER INFORMATION: /F
                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-DAN-91
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                    misc_feature
4471..10722
misc_feature
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1693..2670
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beta-ketoacyl ACP synthase of module
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module 3"
                                                                                                                                                                                                                                                                                                          /function= "approximate span of
acyltransferase domain module 3
                                  /function=
module 4"
                                                                                                                                                                                                             /function= "approximate span of beta-ketoreductase domain of module 3"
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/function= "gene eryA"
/product= "eryA ORF2 er
6-deoxyerythronolide B'
                                                                                                                       /function= "approximate acyl carrier domain of m
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                                                 "approximate span of
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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LOCATION: 15172..16569
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain
FEATURE:
NAME/KEY: misc_feature
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LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
FEATURE:
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OTHER INFORMATION:
FEATURE:
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NAME/KEY: misc_feature
LOCATION: 14062..14610
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LOCATION: 10723..20
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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Conservative

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Claim 6; Fig IA-D; 73pp; English. Chaim 6; Fig IA-D; 73pp; English. This DNA encodes a human DnaJ-like two human DnaJ-like proteins which (HSpyl) and nucleic acid cells containing a vector comprisit production of recombinant proteins to raise Ab, therapeutically and to Antagonists are used to treat or puleukaemia and lymphoma; immune discipled sclero; syndromediabetes mellitus, multiple sclero; and parasitic infections) and infil or prevent tissue damage, e.g. in a strack, ischaemia, UV exposure, in healing, and may be expressed from healing, and may be expressed from trapters of the nucleic acids are detecting and quantifying the HSPJ hybridisation and/or amplification triplex-forming or ribozyme molecusequence 1376 BP; 387 A;	sapiens Sapien	y 1 9 9 06099 standard; DNA; 1376 BP. 0706099; standard; DNA; 1376 BP. 0806099; standard; DNA; 1376 BP. 09-APR-1999 (first entry) 09-APR-1999 (first entry) Human DnaJ-like protein; heat shock immune disorder; inflammation; chromosome manping: ss	3 3 3 3 3 4 4 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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protein, HSPJI. The are heat shock protein sequences encoding by the nucleic acids. Recombinant HSPJI screen for specification of the protein a wide variety revent a wide variety as the nucleic acids is, rheumatoid artinumation. Agonists resultin-dependent dial a vector containing used as primers and encoding nucleic ad assays, therapeutical assays, and for chromoses.	a ara ci arang s	ALIGNMENTS encoding DNA. protein; HSPJ1; HSPJ2; tissue damage; diabete	Q46806 T84330 V72905 V04554 Q50632 T15775 G11710 V90426 V90426 V13834 Q48024
The invention provides roteins J1 and J2 ng the proteins. Host ids are used for the J1 and HSPJZ are used fist binding agents. iety of solid cancers, iety of solid cancers, f many disclosed are f, Crohn's disease, rthritis, microbial s may be used to treat ng spondylitis, heart labetes and for wounding the nucleic acids. and probes for acid in usual acid in usual tically as antisense, mosome mapping.	xaa) xaa)	cancer; leukaemia; s; wound healing;	eryA region of S. Maize DnaJ-related Maize DnaJ clone D DNA encoding a hum Brain factor 2. Is E.coli K12 dnaJ co Dictyostelium plas EST clone DM360. N Human telomerase p Homo sapiens ambig AIGF gene #1. Cell

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rinflammation

PS Claim 27; Fig 3A-D; 73pp; English.

CC This DNA encodes a human DnaJ-like protein, HSPJ2. The invention provides two human DnaJ-like proteins which are heat shock proteins J1 and J2

CC two human DnaJ-like proteins which are heat shock proteins J1 and J2

CC (HSPJ1 and HSPJ2) and nucleic acid sequences encoding the proteins. Host CC production of recombinant proteins. Recombinant HSPJ1 and HSPJ2 are used to traise Ab, therapeutically and to screen for specific binding agents. CC Antagonists are used to treat or prevent a wide variety of solid cancers, leukaemia and lymphoma; immune disorders (typical of many disclosed are acquired immune deficiency syndrome, allergy, asthma, Crohn's disease, CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, microbial cor prevent tissue damage, e.g. in cases of ankylosing spondylitis, heart attack, ischaemia, UV exposure, insulin-dependent diabetes and for wound fragments of the nucleic acids are used as primers and probes for detecting and quantifying the HSPJ-encoding nucleic acid in usual CC hybridisation and/or amplification assays, therapeutically as antisense, triplex-forming or ribozyme molecules, and for chromosome mapping.

271 T;

336 A; 338 C; 338 C; 271 T;
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10-DEC-1998;
02-UUN-1998; U11182.
03-UUN-1997; US-868288.
(INCY) INCYTE PHARM INC.
Au-Young J, Bandman O, Lal
WPI; 99-070259/06.
P-PSDB; W94066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Key
CDS
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DnaJ-like protein; heat shock protein; HSPJ1; HSPJ2; cancer; leukaemia; immune disorder; inflammation; tissue damage; diabetes; wound healing;
                                                                                                                                                                                                                                                                                                                                                                        treatment and prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping;
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/transl_except= (pos:871. 873; aa:Xaa)
/transl_except= (pos:970. 972; aa:Xaa)
/transl_except= (pos:1024. 1026; aa:Xaa)
/transl_except= (pos:1027. 1029; aa:Xaa)
/transl_except= (pos:1033. 1035; aa:Xaa)
/transl_except= (pos:1048. 1050; aa:Xaa)
/transl_except= (pos:1057. 1059; aa:Xaa)
/transl_except= (pos:1060. 1062; aa:Xaa)
/transl_except= (pos:1069. 1071; aa:Xaa)
/transl_except= (pos:1081. 1083; aa:Xaa)
/transl_except= (pos:1081. 1083; aa:Xaa)
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of cancer, immune disorders
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08-OCT-1998.
01-APR-1998; U06371.
29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                                                                                                                                New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 1; Page 853-855; 2054pp; English.

This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and pept ulcer diseases, e.g. gastric and duodenal ulcers. They can also be use for the production of antibodies. The products can also be used for the production of antibodies. The products can also be used for many diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHPO protein; Helicobacter peptic ulcer disease; ss. Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                        detection and diagnosis. Sequence 1204 BP; 4
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                                                   CTCTATAAAGGATATTAAAAAAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCG
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CAACCAAGAGACCATTAAAAAGTCTTACAGAAAGCTGGCTTTAAAATACCACCCAGACAG
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                                                                                                            CATTTTTGGAGCGATCGTGGAATTGAGTTATTATGAAATTTTAGAAGTGGAAAAACACAG
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8.5e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis Claim 1; Page 210-227; 1150pp; English.

**R20500-21243** represent polynucleotide sequences from the genome of X20500-21243 represent polynucleotide sequences for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detection diseases related to Borrelia infections in animals, and for the production of biosynthetic products such as enzymes.

Sequence 28295 BP; 6269 A; 6077 C; 8919 G; 696 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1998.
30-DEC-1998; U13041.
23-JUN-1998; US-050667.
24-JUN-1997; US-050667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum inf enzyme production; ds.
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Fraser CM;
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                                                                                        GATGGTCA
                                                                                                                                                                                                                                                                 GCCTCTATAAAAGGATATTAAAAAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGAC
                                                                                                                                                                                                                                                                                                             CTAGACGGGGTGATCGTGGCAAAGAAGGATTATTACGAGGTTCTCGGTATCTCAAAGACC 26763
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                                                           GATATGCA
                                                                                                                        GTGCTCATTGATGCACAGAAGCGTGCCGCGTACGATCGGTATGGCTTTGATGGCCTGAAG
                                                                                                                                                    GTTCTGTCAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAAGGATTAAAA 480
                                                                                                                                                                                                                 CGGAACCCTGATGATCCACAAGCCCCAGGAGAATTCCCAGGATCTGGGTGCTGCTTATGAG
                                                                                                                                                                                                                                              GTTTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                     4.9%;
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Pred. No. 2.6e-08;
0; Mismatches 113
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Best Local :
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23-JUN-1994; US-265100.
(STRD) UNIV LELAND STAN
Bloom D, Fathman G;
WPI; 96-068884/07.
              Human cysteine string protein gene.
Human; cysteine string protein; anergy; T-lymphocyte;
differential display; cDNA; reverse transcription; probe
polymerase chain reaction; cloning; gel electrophoresis;
                                                                                                                07-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying genes associated with T-cell anergy, and the protein encoded by them - useful to elucidate the anergic state, and identify agents associated with induction of anergy

Disclosure; Fig 2; 31pp; English.

The sequence encodes a mouse cysteine string protein isolated from mouse T-cell clones 11.3.7 and 12.2 by a new procedure for identification of genes associated with anergy. The protein is expressed in restling T-cells but not in anergic T-cells. To isolate proteins of this type, differential display is first performed by generating CDNA from polyA+ mRNA with an oligo-dr primer with 2 variable anchor nuclostides at the 3'-end, e.g. mail of the contact of the cont
                                                                                                                                                                 T11789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fil786, using reverse-transcriptase. The resulting cDNA populations are amplified by the polymerase chain reaction, using the same oligo-dT primer and a 5'-primer which includes common 4-5 nucleotide sequence combinations, e.g. Til785. After gel electrophoresis of the products, bands unique to anergised or non-anergised cells are excised, eluted, amplified, cloned and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequenced. Genes and proteins (and corresponding antibodies) arising from this procedure may be used e.g. in monitoring autoimmune disease, organ transplantation, vaccine
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Sequence 672
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                                                                                                                                                                                                                                                                                    211
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WO9600300-A1.
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immunoassay; autoimmune
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Pred. No.
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1.5e-08;
90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence encodes a human cysicine string protein, the absence of which is associated with anergy in T-cells. Genes with at leas 20 Me which is associated with anergy in T-cells. Genes with at leas 20 Me with a probes for detection of the anergic state, and may be 20 used as probes for detection of the anergic state, and may be 21 merformed by generating cDNA from polyA+ mRNA with an ollgo-dr 22 primer with 2 variable anchor nucleotides at the 3'-end, e.g. 21 mer with 2 variable anchor nucleotides at the 3'-end, e.g. 21 mer with 2 variable anchor nucleotides at the 3'-end, e.g. 21 mer with 2 variable anchor nucleotides at the 3'-end, e.g. 21 mer with 2 variable anchor nucleotides at the 3'-end, e.g. 21 mer with 1 mer and 2 mergised or 2 using the same oligo-dr primer and a 5'-primer which includes 2 common 4-5 nucleotide sequence combinations, e.g. 211785. After 2 common 4-5 nucleotide sequence combinations, e.g. 211785. After 2 common 4-5 nucleotide sequence was bands unique to anergised or 2 non-anergised cells are excised, eluted, amplified, cloned and 2 sequenced. Genes and proteins (and corresponding antibodies) autoimmune disease, organ transplantation, vaccine 2 effectiveness, and in drug screening.

Sequence 672 mer and in drug screening.
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Best Local
                                                                                                                                      Homo sapiens.
WO9403599-A.
17-FEB-1994.
                                                                          04-AUG-1993;
04-AUG-1992;
13-NOV-1992;
26-FEB-1993;
   P-PSDB;
cDNA of
                               Iwahori
WPI; 94
                                                                                                                                                                              DNA J like protein.
Human cDNA; library; enzyme; protein;
                                                            (SAGA)
                                                                                                                                                                                                             19-OCT-1994 (first entry)
                                                                                                                                                                                                                                             Q57429 standard; cDNA
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23-JUN-1994;
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                               A ) SAGAMI CHEM RES CENTRE. ori A, Kato S, Kato T, Kim 94-065688/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
119; Conser
                    R46090
                                                                          ; J01095.
; JP-208077.
; JP-327619.
; JP-061431.
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US-265100.
   origin
   and
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   proteins
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Pred.
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Claim 1; Page 44-47; 167pp; Japanese.

mRNA expressed in human fibrosarcoma cell line HT-10 isolated and used to construct a CDNA library using pXA1. Clone HP00067 encoding DNA J-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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X20248_08
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                                                                                                                                                              TTATAGAAAAATAGCAATTAAATATCACCCAGÁCAGAAATCAAGGGAATGAAGAAGCCGC
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Pred. No. 9.4e-08;
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Pred. No. 3.5e-06;
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29-JUN-1998; U13530.
30-JUN-1997; US-885610.
(GEMY ) GENETICS INST INC.
Agostino MJ, Evans C, Jacobs K
Merberg D, Racie LA, Treacy M;
WPI; 99-095571/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                 15446 ATTTAGCAGCACAAGATTTGGCAATTTTG
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          The sequence is that encoding a secreted protein from a human fetal kidney clone AM610. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth activity, haemost activin/inhibin activity, chemotactic/chemokinetic activity, haemost
                                                                                          Disclosure; Pages 55-56; 76pp; English. The sequence is that encoding a secrete kidney clone AM610. Such a sequence is
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x07570;
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or C

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PT New polynucleotides encoding human secreted proteins - derived from PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, PT ovary, pituitary, retina and coolon cDNA libraries
PS Claim 1; Page 234; 633pp; English.

CC This sequence represents an expressed sequence tag (EST), and is a CC polynucleotide of the invention. The polynucleotides of the invention are CC all secreted EST sequences isolated from a variety of human tissue CC sources. The EST sequences and proteins encoded by them are predicted to CC treating, preventing or ameliorating medical conditions in humans and CC animals, although no supporting data is given. Suggested activities of include nutritional activity, immune stimulating or suppressing activity, family, land activity, haemostatic CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
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Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                        Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg Racie LA, Spaulding V, Treacy M; WPI; 99-070076/06.
                  therapy
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10-APR-1998; U06954.
10-APR-1997; US-835913.
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WO9845435-A2.
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Sequence
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inhibition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCATTTTAATGATAACAGAATTAATTCTGGCCTCAAAAAGCTACTATGATATCTTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cadherin/tumour invasion suppressor activity, and tumour activity. It is also stated to be useful for gene
   331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1726 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%;
   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 A;
   Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59.2; DB 1;
Pred. No. 9.9e-07;
D; Mismatches 153;
 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 C;
ü
 8
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1726
79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вþ
                                                                                                                                                                                                                                                            responsible for antiviral agents which have little effect on mon-infected cells - by determining whether the agent interacts with a virus or cellular component and allows or prevents referential translation of viral RNA.

Example 6; Page 168-69; 195pp; English.

This sequence represents the influenza virus p58 cDNA. This sequence was isolated using probes based on tryptic peptides derived from p58.

These probes were used to screen a cDNA library from MDBK cell line made in lambda Zap II vector. The initial clone contained a long open reading frame but no termination codon suggesting that the 3' end was missing. The 3' end was isolated by RACE-PCR. This allowed construction of the full length p58 cDNA containing 1680 bp.

Sequence 1515 BP; 509 A; 285 C; 362 G; 359 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
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                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
    1295
                                                                   1235
                                                                                                                               1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9423041-A.
13-OCT-1994.
01-APR-1994; U03623.
02-APR-1993; US-042024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katze MG, Mathews WPI; 94-333201/41.
                                                                                               323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza virus; p58; probe; MDBK cell line; RACE-PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p58 cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q77721 standard; cDNA; 1515
                                    380
                                                                                                                                            263 GACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 GACGAAAAGAGTATGATACACTTGGACACAGTGCTTTTACTAGTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 AACGGAAACAGTACGATACTTATIGGTGAAGAAGGATTAAAAGATGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 CTCCGCAGAACCTGAGCACCTTTTGCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
AGAAAAAAGCTGAGAAGAAGTTCATTGACATAGCAGCTGCTAAAGAAGTCCTCTCCGATC
                                                                                          AGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGATCCAC---
                                                                                                                          GACGAGATTATTACAAAATCTTGGGAGTAAAAAGAAATGCCAAAAAAGCAAGAAATCATTA 1234
                             -----AAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATA
                                                              AAGCATACCGAAAATTAGCACTGCAGTGGCACCCAGACAACTTCCAGAACGAAGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTGAGA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCTGAAGCAAAATTCAGAGAGATTGCAGAAGCATATGAAACACTCTCAGATGCTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAGGCCTTTCACAAGTTGGCCATGAAGTACCACCCTGACAAAAA----TAAGAGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGGACCGGAACCCTGATGATCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCAAAAAGCTACTATGATATCTTAGGTGTGCCAAAATCGGCATCAGAGCGCCAAATCA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIBOGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mathews MB,
                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                        3.98;
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52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miles VJ,
                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                     Score 53.4; DB 1;
Pred. No. 3.7e-05;
0; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB 1;
Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watson JC,
                                                                                                                                                                                         76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Witherell G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 331
                                                                                                                                                                                                                      Length 1515;
                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321
                                                                                                                                                                                                                                                                                                                                                                           This sequence
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                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                           p58
                                                            1294
                                                                                           380
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RESULT
V22052
ID V2
AC V2
DE BC
C KW BC
ON BC
PD 114
PP 01
PP 01
PP 01
PP 07
PP 07
PP 07
PP 1 KK
PP 1 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 118
US5670330-A.
23-SEP-1997.
25-OCT-1993;
25-OCT-1993;
29-SEP-1992;
22-OCT-1993;
(UYMC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine; p58;
Bos taurus.
US5738985-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIBO-) RIBOGENE INC.

Katze MG, Mathews MB, Miles VJ;

WPI; 98-260029/23.

Screening assays for antiviral agents - l

translation, protein kinase activity, etc

Example 6; Columns 85-88; 65pp; English.
                                                                                                                                                                                                                                                                                                                                              Bovine
Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-1998.
01-APR-1994; 221816.
01-APR-1994; US-221816.
02-APR-1993; US-042024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1235
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Sequence 1
                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                V01072
                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                             V01072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                          taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGAGATTTCTATAAGATCTTGGGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGAGAAACGGAAACAGTACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGGACCGGAACCCTGATGATCCAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAAATGAGGAAGAAGTTTGAT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAGAAACGGAAACAGTACGAT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAAATGAGGAAGAAGTTTGAT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCATACCGAAAATTAGCACTGCAGTGGCACCCAGACAACTTCCAGAACGAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAAAAAAGCTGAGAAGAAGTTCATTGACATAGCAGCTGCTAAAGAAGTCCTCTCCGATC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
118; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p58
                                                                                                                                                                                                                                                                                                                               PKR; double stranded RNA-activated protein kinase; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p58; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1515 BP;
  143219.
US-143219.
US-953681.
US-141244.
V MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                             differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B₽;
                                                                                                                                                                                  /transl_except=
1626. .1631
                                                                                                                                             /*tag=
/note=
                                                                                                                                                                                               /*tag= a
/product= P58_protein
/=-n=1 except= (pos:
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
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                                                                                                                                                                                                                                                                  .1630
                                                                                                                                                                                                                                                                                                                                                                                                                                1687
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                                                                                                                                          "sub-optimal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bovine p58 DI
509 A; 285
                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 53.4; D
; Pred. No. 3.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456
                                                                                                                                                                                                                                                                                                                           tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA.
85 C;
                                                                                                                                             polyA signal
                                                                                                                                                                                                                                                                                                                           suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             etc.
                                                                                                                                                                                                          365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7e-05;
1es 76;
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                                                                                                                                                                                                       .367,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362
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                                                                                                                                                                                                                                                                                                                             tumourigenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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This is the nucleotide sequence of the gene encoding the bovine P58 protein, a cellular 58 kD protein purified from influenza-infected cells. The protein is used to reduce the activity of a PKR protein (e.g. W36139) in a screening method for identifying anti-tumour agents by measuring PKR activity in a system before and after adding a test agent, where an increase in PKR activity indicates that the agent is an anti-tumour agent, especially useful for the prevention and/or treatment of neoplasms. PKR is an interferon-inducible cytoplasmic Ser-Thr specific protein kinase which can also be activated by double stranded RNA. PKR is active in cell growth and differentiation by regulating protein synthesis, and thus has been suggested to function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIW ) UNIV WASHINGTON Barber GH, Katze MG, Kol WPI; 97-479453/44.
                                                                                                                                                                                                                                                                                                           Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
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Claim 1; Page 969-972; 3271pp; English.

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences

CC of the invention. The DNA sequences are recorded on a computer readable

CC medium, preferably selected from a floppy or hard disk, random access

CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using

CC that protein-encoding or regulatory regions of commercial, therapeutic or

CC industrial importance can be obtained. Specifically, sequences which are

CC likely to encode antigens have been identified and these polypeptides can

CC saureus in a sample. Saureus infection. The

CC saureus in a sample. Saureus is implicated in numerous human diseases,

CC skin and surgical wound infections, scalded skin syndrome, toxic shock

CC syndrome, etc. Organisms transformed with the DNA sequences can be used

CC (and their fragments) are useful as primers or probes for isolating

CC computer readable medium.

Secuence 6336 NP: 1733 A. 1318 G. 2026 M. 2026 M.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 123; Conserv
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                                                                                                                                                 3111
                                                                                                                                                                                                            3171 TGGCCAAAAGAGATTATTATGAAGTTTTAGGCATTAGTAAGGATGCTTCAAAAGATGAAA 3112
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30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                         437
                                                                                                                377
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ATAAACGCGCAAGCTATGATCAATTTGGACATGATGGTCCACAAGGT 2948
                    AGAAACGGAAACAGTACGATACTTATGGTGAAGAAGGATTAAAAGAT 483
                                                                                                                                                                  TTAAAAAGGCCTATAGGAAACTAGCCCTGCAGCTTCATCCCGACCGGAACCCTGATGATC 376
                                                                   -AGGTGCAGATGAAAAGTTTAAAGAAATTTCTGAAGCCTATGAAGTTTTAAGTGATGATA 2995
                                                                                         CACAAGCCCAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTG 436
                                                                                                                                        TCAAAAAAGCGTATCGAAAGCTTTCGAAAAATATCATCCAGATATTAACAAAGAAGA--
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Search completed: June 30, 2000, 14:10:37 Job time: 8104 sec

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atc cal	OB-868-288A-3 sequence 3, Appli, attent No. 592256 GENERAL INFORMATION APPLICANT: Au APPLICANT: Au APPLICANT: Ba TITLE OF INVEN NUMBER OF SEQU CORRESPONDENCE ADDRESSEE: STREET: 317 CITY: Palo. STATE: CA COUNTRY: US. COMPUTER READA MEDIUM TYPE: COMPUTER: IT OPERATING SY, SOFTWARE: FILING DATE: COMPUTER: IT OPERATION FILING DATE: PRIOR APPLICATION FILEFAX: 41 INFORMATION FOR SEQUENCE CHARA LENGTH: 330 TYPE: amino STRANDEDNESS TOPOLOGY: I IMMEDIATE SOUR LEBRARY: HN CLONE: 2608 08-868-288A-3		147 110.5 110.5 110.5 103.5 103.5 103.5 103.5 103.5 96.5 96.5
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Patent No. 6001598
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                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/868,288
FILING DATE: June 3, 1997
ATTORNEY/ACENT INFORMATION:
NAME: B1111ngs, Lucy J.
REFERENCY/ACONOMINER: 36,749
REGERENCY/ACONOMINER: 36,749
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: 415-855-0555
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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CITY: Palo Alto
                                                                        LIBRARY: HNT2R
CLONE: 260873
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APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
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3174 Porter Drive
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Score 1696; DB 3;
Pred. No. 2.9e-167;
            Length 330;
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RESULT 3
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                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Au-Young, Janice
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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IMMEDIATE SOURCE:
LIBRARY: HNT2R
CLONE: 260873
                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                 TOPOLOGY:
                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                330 amino acids
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              HNT2RAT01
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                                               linear
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DB 2; 48;

277;

Indels Length

41;

Gaps

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-GH---SDF 150

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RESULT 4
US-08-868-288A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 330; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08 FILING DATE: June 3, 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: JA.,
CITY: Palo Alto
STATE: CA
STATE: TCA
                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
IMMEDIATE SOURCE:
LIBRARY: GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                 amino acid
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                                                                                     277 amino acids
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                                linear
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pred. No. 2.9e-167;
                                                                                                                                                                                                   PF-0309 US
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US-08-868-288A-7
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US-09-235-373-7
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Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Approximately No. 6001598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olya
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/868,28

APPLICATION NUMBER: 31,997

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
                                                                                                                                           TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
             IMMEDIATE SOURCE:
LIBRARY: GenBa
                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 POR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KREIYDRYGREGLTGTGTSPSRAEAGSGGPGFTFTFRSPEEVFREFFGSGDPFA-ELFDD 119
                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/235,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                             08/868,288
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us-09-235-373-7

Query Match 37.0 Best Local Similarity 54.4 Matches 142; Conservative

37.08;

Score 635.5; DB 3 Pred. No. 7.2e-58;

DB 3; 48;

Length Indels

277; 41;

Query Match Best Local :

Local

Similarity

DB ω --

Length

277;

9;

Gaps

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30; Mismatches

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DLARGLELSRREQ-----QPS

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151 176 ş B Ş

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118

120 LGPFSEL--QNRG-----SRHSGPFFTFSSSFP-----

SSTSFGGS-GMGNFKSISTSTKMVNGRKITTKRIVENGQERVEVEEDGQLKSLTINGVAD

SSSSFSFSPGAGAFRSVSTSTTFVQGRRITTRRIMENGQERVEVEEDGQLKSVTINGVPD

210 234 150 61 KREIYDRYGREGLIGIGTGPSRAEAGSGGPGFTFTFRSPEEVFREFFGSGDPFA-ELFDD

KRDIYDKYGKEGLNGGGGGGSHFDSPF---EFGFTFRNPDDVFREEFFGGRDPFSFDFFED 117

--PFEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSF 175

--GH---SDF

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; CLONE: US-09-388-993-7
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                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Au-You
           IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 32470
                                                                                                                                                                                                                                                                                                          FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                                                            STRANDEDNESS:
                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                              GenBank
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US-08-868-288A-6
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GENERAL INFORMATION:
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                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY BILLINGS, LUCY J.
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
          IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 32469
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UFILING DATE: June 3, PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
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                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 LGPFSEL--QNRG----SRHSGPFFTFSSSFP---
                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                          ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
                                                                                        amino acid
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                                                                                                          351 amino acids
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3174 Porter Drive
                                                                                                                                                           415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
SYSTEM: DOS
FastSEQ for Windows Version
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                                                          linear
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                                                                                                                                                                                                         PF-0309
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US-09-235-373-6
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Patent No. 6001598
GENERAL INFORMATION:
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                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/868,288
FILING DATE: June 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 95-0309 US
REFERENCE/DOCKET NUMBER: PF-0309 US
                                                                                                                                      TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                          IMMEDIATE SOURCE
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LIBRARY: GELL
CNE: 32469
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                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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Patent No. 604322
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Best Local Similarity
                                                                                                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                      TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                 SEQUENCE CHARACTERISTICS:
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MMEDIAL
LIBRARY: General
NR: 32469
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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                                                                    STRANDEDNESS:
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                                                                                                 351 amino acids
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54.48;

32.9%;

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US-08-974-546-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 142; Conserva
                                                                                                     TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                          IMMEDIATE SOURCE:
                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,546
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 LGPFSEL--QNRG-----SRHSGPFFTFSSSFP-------GH---SDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 DDALXEERMRRGQNVLPAQPA 255
                                            TOPOLOGY:
                                                         STRANDEDNESS:
                                                                          TYPE: amino acid
           LIBRARY:
                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KRDIYDKYGKEGLNGGGGGGSHFDSPF---EFGFTFRNPDDVFREFFGGRDPFSFDFFED 117
                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVDYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLARGLELSRREQ-----QPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSTSFGGS-GMGNFKSISTSTKMVNGRKITTKRIVENGQERVEVEEDGQLKSLTINGVAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASYYEILDVPRSASADDIKKAYRRKALQWHPDKNPDNKEFAEKKFKEVAEAYEVLSDKH 60
                                                                                                                                                                                                                                                                                                                                                                                                                 94304
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: CA
: GenBank
1816452
                                                                                       340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
                                                                                                                                     650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillman,
                                            linear
                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jennifer L.
                                                                                                                       5
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                                                                                                                                                                                 PF-0428
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Query Match

21.2%;

Score 364.5;

DВ

2.

Length 340;

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RESULT 11
US-08-974-546-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 32.9
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                TELEPHONE: 650-855-05
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEF: To CORRESPONDENCE ADDRESS:
             TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 31/.
OTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 G 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 NVNFGRS-----RSAQEPARKKQDPPVT------HDLRVSLEEIYSGCTKKMKISHKRL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 STSFGGSGMGNFKSISTSTKMVNGRKITTKRIVENGQERVEVEE--DGQLKSLTIN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 NPFDTFFGQRNGEEGM-----DIDDPFSGFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 DPFEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSFS 176
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                              STRANDEDNESS:
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 EIFDRYGEEGLKGSGPSGGSGGANGTS---FSYTFHGDPHAMFAEFFGGR----- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DYYQTLGLARGASDEEIKRAYRRQALRYHPDKNKE--PGAEEKFKEIAEAYDVLSDPRKR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GVADDDALXEERMRRG-----QNVLPAQPAGLRPPKPPRPASLLRHXPHCLSKEE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                      94304
                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08974546
                                                                            348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3174 Porter Dr.
                                                                                                                                    650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley, Neil C.
Shah, Purvi
BRAITUT21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lal, Preet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillman, Jennifer L.
                                 linear
                                                                                                                                                   650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                single
                                                                                                                                                                                                                                                                                                                     US/08/974,546
                                                                                                                                                                                                  36,749
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                                                                                                                                                                                    PF-0428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9.2e-30; 6; Mismatches 81;
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US-08-974-546-1

Matches Query Match Best Local

Local Similarity nes 96; Conserv

Conservative

39;

Mismatches

101;

62;

Gaps

11;

Length 348;

19.6%; Score 337; DB 2; 32.2%; Pred. No. 6.6e-27;

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US-08-868-288A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Au-xoury, APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: BANDMAN, DNAJ-LIKE PROTEINS
                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0309 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/868,288A FILING DATE: June 3, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                    TOPOLOGY: line
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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  MEDIAL GELL
LIBRARY: GELL
ONE: 306714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GLYDQYGEEGLKTGGGTSGG----SSGSFHYTFHGDPHATFASFFGG-----SNPF 108
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                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 DYYKILGIPSGANEDEIKKAYRKMALKYHPDKNKE--PNAEEKFKEIAEAYDVLSDPKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIFFASSRSTR------PFSGFDPDDMDVDEDEDPFGAFGRFGFNGLSRGPRRA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRTVRTEDKILHIVIKRGWKEGTKITFPKEGDATPDNIPADIVFVLKDKPHAHFRRDG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGGSGMGNFKSISTSTKMVNGRKITTKRIVENGQERVEVEE--DGQLKSLTI------
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                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3174 Porter Drive
                                                                                                                              397 amino acids
                                                                                                                                                                                          415-845-4166
                                    GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                          linear
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                                                                                                                                                                                                             415-855-0555
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US-09-235-373-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09235373
Patent No. 6001598
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Lal, Preeti
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                                                                                                          TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
                                                                                                                                                                                                                             APPLICATION NUMBER: 08/868,2
FILING DATE: June 3, 1997
ATTORNEY_AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                    TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                      FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                               IMMEDIATE SOURCE:
 LIBRARY: GE...
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                                                                   TOPOLOGY:
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
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                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
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                                                                                                 amino acid
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                                 GenBank
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for Windows Version
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32.8%;
                                                                                                                                                                                                                                                                                                      08/868,288
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Pred. No. 3.8e-24;
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CLONE:
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Best Local S
Matches 88
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                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
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                                          STRANDEDNESS: S
TOPOLOGY: linea
IMMEDIATE SOURCE:
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
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TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
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              LIBRARY: GenBank
CLONE: 306714
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                                                                                                   amino acid
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IBM Compatible
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                                                                                 single
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32.8%; Pred. NO. 3.8e-24;
30. Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                            US/09/388,993
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; MOLECULE TYPE: protein US-08-686-417-3
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GENERAL INFORMATION:
APPLICANT: Baszcz
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Best Local Similarity
                                                                                                            TELEFAX: (202) 822-0168 INFORMATION FOR SEQ ID NO:
                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acid:
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: AN TITLE OF INVENTION: GE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 26-JUI
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                                       TOPOLOGY:
                                                                                                                                                TELEPHONE:
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                         CLASSIFICATION:
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5850018
                                                                       419 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Rosichan, Jeffrey 1
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Pred. No. 3.8e-24;
0; Mismatches 72
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Matches

Conservative

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Mismatches

.4e-20; DB 2;

Length 419; Indels

35;

Gaps

5.

Query Match Best Local Similarity

16.0%; Score 274.5; 45.9%; Pred. No. 2.4

Human Human

Human

Human

protein

Human Human Human Human Human Human

leukaemia;

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d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being prin
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                                                                                        nucl
 New nucleic acid encoding human DnaJ-like proteins - for diagnosis, treatment and prevention of cancer, immune disorders and inflammation claim 22; F1g 3A-D; 73pp; English.

This represents a human DnaJ-like protein, HSpJ2. The invention proves two human DnaJ-like proteins which are heat shock proteins J1 and J3 (HSpJ1 and HSpJ2) and nucleic acid sequences encoding the proteins. cells containing a vector comprising the nucleic acids are used for
                                                                    Au-Young J, Bandman O, Lal
WPI; 99-070259/06.
N-PSDB; X06100.
                                                                                              10-DEC-1998.
02-JUN-1998; U11182.
03-JUN-1997; US-868288.
(INCY-) INCYTE PHARM IN
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DnaJ-like protein; heat shock protein;
immune disorder; inflammation; tissue of
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US-09-501-714-3 1716

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01-APR-1998; U06371.

29-JUL-1997; US-902615.

01-APR-1997; US-833457.

24-JUN-1997; US-881227.
New isolated Helicobacter polynucleotides - used to develop product for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 8; Page 853-855; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating the invention. The polypeptides can be used for preventing or treating invention.
                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUNS.
Al-Gdarawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. pylori GHPO 885 protein.
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
Helicobacter pylori.
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    I specific promoters, partic. for control of antifungal and insecticide genes

S Example 1; Fig 2A-B; 26pp; English.

C This polypeptide sequence is encoded by the maize DnaJ-related gene (see T8430). DnaJ-related proteins assist in chaperone-mediated protein folding and provide cell viability at high temperatures. They are also involved in DNA replication, translation and peptide translocation across intracellular membranes. Due to this wide range of functions, DnaJ has a wide range of effectiveness and the gene spromoter sequence, ZmDJI (see T84329), is effective in a wide range of tissues. The claimed ZmDJI promoter can be used in claimed methods for control of antifungal or insecticidal genes in transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Ma
Best Loc
Matches
                                                                                                                                                                                   Tobacco DnaJ-related gene transcription/translation regulatory sequence, ZmDJI - is intermediate between constitutive and tiss specific promoters, partic for control of antifungal and
                                                                                                                                                                                                                                                                                                                                                                          DnaJ-related protein; chaperone; protein folding; DNA replication; translation; peptide translocation; ZmDJ1; promoter; maize; transgenic plant; insecticide; antifungal; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              these infections, including peptic ulcer diseases, e.g. used for the production of a paraction and diagnosis.
                                                                                                                                                                                                                                                                       12-JUL-1996; U11676.
26-JUL-1995; US-001522.
(PION-) PIONEER HI-BRED
                                                                                                                                                                                                                                 N-PSDB; T84330
                                                                                                                                                                                                                                                               Barbour E,
                                                                                                                                                                                                                                                                                                                                                              crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                        Maize DnaJ-related protein.
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                                                                                                                                                                                                                                             our E, Baszczynski
97-145697/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEDAFG--FGARGSKRQKSSIAPDYLQTLELSFKEAVFGCKKTIKVQYQSVCESCDGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDIYDKYGKEGLNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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93; Conserv
 419
                                                                                                                                                                                                                                                                                                                                                  CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AA;
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                                                                                                                                                                                                                                                                                                                                                   В73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DEEIDAIIPEGIDDQNRMVLKNKGNEYEKGKRGDLYLEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                including acute, chronic, and atrophic gastritis, ases, e.g. gastric and duodenal ulcers. They can a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%;
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                                                                                                                                                                                                                                                            Horowitz
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Pred. No. 1e-21;
2; Mismatches
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                                                                                                                                                                                                                                                              Rosichan
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                           control
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Query Match Best Local S Matches 62

Similarity

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Score 274.5; Pred. No. 6.16 5; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The present invention describes the maize ZMDJI control sequence. Also control sequence linked to a heterologous protein coding sequence: ZMDJI control sequence linked to a heterologous protein coding sequence: CC (2) a monocotyledonous plant, plant part or plant cell modified to control sequence which retain transcription-initiating activity and/or CC contain the expression system; (3) DNA comprising fragments of the ZMDJI control sequence which retain transcription-initiating activity and/or CC the function of the leader sequence; and (4) a method to regulate the cc expression of a gene under control of the ZMDJI control sequence in CC plant cell, plant parts or plants, where the plant is a monocotyledon, CC comprising modifying the cell, part or plant containing the gene under CC control of the ZMDJI control sequence to contain the DNA of (3) or RNA CC of the same nucleotide sequence. Expression systems as described above in which the heterologous sequence encodes an insecticidal or antifungal CC insects (e.g. European corn borer) or fingi (e.g. Ostrinia nubilalis). CC The control sequence comprises a constitutive promoter that directs transgene expression in various plant tissues, including II-week-old CC leaf blades, leaf whorls, leaf collars, stalk rind, stalk pith, stalk condes, roots and kernels. The present sequence represents the protein cencoded by a maize DnaJ clone from the present invention.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize ZMDJ1 promoter - and consystems and transgenic plants Example 1; Fig 2; 16pp; Englis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize DnaJ clone protein sequence.
Maize; Zea mays; transcriptional promoter; control sequence;
DnaJ clone; corn; insecticide; antifungal protein; transgenic
insect resistance; European corn borer; fungal resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barbour E, Baszczynski C, WPI; 99-069853/06.
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Barbour E, Baszczynski (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1996; 686417.
27-JUL-1995; US-001552.
26-JUL-1996; US-686417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5850018-A.
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23-FEB-1999
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                                                                                                                                                                                                                   4 YYEVLGVQRHASPEDIKKAYRKLALKWHPDK--NPENKEEAERKFKQVAEAYEVLSDAKK 61
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DFFGNRRGPRGSRSR 135
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                                                                                                                         RDIYDKYGKEGLNGG-GGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDPFE 120
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45.9%;
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                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                          Score 274.5; DB 1
Pred. No. 6.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                             35;
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                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a secreted protein from a human fetal kidney clone AK296. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemostation activity, chemotactic/chemokinetic activity, haemostatiand thrombolytic activity, receptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene
             Streptococcus W09640928-A1.
                                          open
E. co
                                                                   s. pneumoniae
streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agostino MJ, Evans C, Jacobs
Merberg D, Racie LA, Treacy N
WPI; 99-095671/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potential vaccines
Claim 13; Pages 56-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; X07570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens feta 
Secreted protein;
                                                                                                     01-OCT-1997
                                                                                                                               W22358 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-1998;
30-JUN-1997;
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                                                                                                                                                                                                                                                                                                                           85
                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                    27
                                         coli; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                 4
                   or, 1997 (first entry)
TT-1997 (first entry)
neumoniae N-terminal portion of DnaJ protein,
ptococcus pneumoniae; S. pyogenes; S. agalactiae; genome; HSP72;
ptococcus pretame; heat shock protein 72; DnaJ; DnaK; chimaeric;
reading frame; heat shock protein 72; DnaJ; DnaK; chimaeric;
roli: Lactococcus lactis; antibody; vaccine; infection; human.
                                                                                                                                                                                                                                      FGGSGMGNFKSISTSTKMVNG----RKITTKR
                                                                                                                                                                                                                                                                                                                                                                                                          YYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKRD 63
                                                                                                                                                                                                                                                                                                                                                      IYDKYGKEGLNGG----GGGGSHFDSPFEFGFTFRNPDDVFREF-FGGRDPFSFDFFEDPF 119
                                                                                                                                                                                                                                                                                                                                                                                    YYDILGVPKSASERQIKKAPHKLAMKYHPDKN--KSPDAEAKFREIAEAYETLSDANRRK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          solynucleotides encoding secreted foetal kidney or adult retina cDN
                                                                                                                                                                                                          FSGFDSTNQHTVQTENRFHGSSKHCRTVTQRR
                                                                                                                                                                                                                                                                 ENHFQTRQDGGSSRQR---HHFQEF----
                                                                                                                                                                                                                                                                                              EDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSFSSTS 179
                                                                                                                                                                                                                                                                                                                           EYDTLGHSAFTSGKGQRGSGSSFEQSFNFNF-----DDLFKDFGFFGQNQNTGS--KKRF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-885610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Æ,
                                                                                                                                Protein; 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetal kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone AM610 secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 272; DB 1;
Pred. No. 4.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ζ,
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                                                                                                                                                                                                                                                                   SFGGGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA libraries, used as, e.g.
                                                                                                                                                                                                                                      207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ER, Mccoy
                                                                                                                                                                                                                                                                    - FDDMFEDMEKM - - :
                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pri used in the production of a vaccine to treating and preventing
Pri strain-specific Streptococcal infection
PS Example 3; Page 93-94; 156pp; English.

CC This amino acid sequence corresponds to the N-terminal portion of the
CC Streptococcus pneumoniae DnaJ protein. The protein shows a high degree
CC of identity (72% and 51%) to the DnaJ proteins from Lactococcus lactis
CC and E. coli respectively. The sequence encoding this truncated protein
CC was isolated on the same nucleotide sequence that encodes the
CC informent was isolated from a HindIII-partially digested genomic DNA
CC ilbrary using a fragment of the chimaeric gene (773392) corresponding to
CC the sequence encoding the C-terminal 16% amino acids of HSP72. The HSP72
CC protein and its fragment, or antibodies specific to HSP72, are used in
CC pharmaceutical compositions, pref. a vaccine, for treating or preventing
CC infection by S. pneumoniae or related bacteria in humans, e.g.
SO Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
W09855509-A2.
10-DEC-1998.
02-JUN-1998; U03-JUN-1997; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995; US-472534.
04-AUG-1995; US-001805.
(IAFB-) IAF BIOVAC INC.
Brodeur B, Hamel J, Mai.
WPI; 97-052328/05.
N-PSDB; T73388.
                                                                                                                                                                       Human DnaJ-like protein, HSPJ1.
DnaJ-like protein; heat shock protein; and shock protein; heat shock protein; inflammation;
                                                                                                                                                             chromosome mapping.
                                                                                                                                                                                                               W94065 standard; Protein; W94065; 09-APR-1999 (first entry)
                                                                                Misc_difference
                                                                                                                       Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1996;
07-JUN-1995;
04-AUG-1995;
                                                                                                                                                   Omo
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                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                              --VETGQQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAYDQYGAAGANGGFGGAGGFGG-FNGAGGFGGFEDIFSSFFGGGGSSRNPNAPRQGDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIYDKYGKEGLNGGGGGSHFDSPFEFGFTFRNPDDVFREFFGG----RDP-----
                                                                                                                                                                                                                                                                                                                                       RIVENGQE 214
                                                                                                                                                                                                                                                                                                                                                              VDTQ-TPLGMMRRQVTCDVCHGRGKEIKYPCTTCHGTGHEK-QAHSVHVKIPAG-----
                                                                                                                                                                                                                                                                                                                                                                                               FDTGFTSFGSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FSFDFFEDFFEDFFGNRR------GPRGSRSRGTGSFFSAFSGFPSFGSGFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFYDRLGVSKNASADEIKKAYRKLSKKYHPDINKE--PGAEDKYKEVQEAYETLSDDQKR
U11182.
US-868288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                299
                                                                                                                       Location/Qualifiers 298
                                                     /note=
                                                                 /label-
                                                                                            note-
                                                                                                          'label=
                                                                                                                                                                                                                                                                                                                                                                                                                    -EAIFGTEKEVKYHREAGCRTCNGSGAKPGTSPVTCGRCHGAGVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%;
32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin
                                                                                            "encoded
                                                   "encoded by
                                                                  unknown
                                                                                                       unknown
                                                                                                                                                                                                     HSPJ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins
                                                                                                                                                                                                                                            358
                                                                                                                                                                                                                                                                                                                                                                                         -GHGGLTSFSSTSFGGSGMGNFKSISTSTKMVNGRKITTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 259.5; DB 1;
Pred. No. 1.6e-18;
30; Mismatches 82;
                                                                                                                                                                       protein; HSPJ1;
; tissue damage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ü
                                                                                                                                                                     HSPJ2; cancer; leukaemia;
diabetes; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Y07061
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Contain it Fig la-D; Englis
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Best Local S
Matches 60
                                                                                                                                                    28-JAN-1999.
15-JUL-1998; U14679.
22-JUN-1998; US-102322.
17-JUL-1997; US-896164.
10-OCT-1997; US-61765.
10-OCT-1997; US-948705.
11-OCT-1997; US-948705.
11-OCT-1997; GB-021697.
(LUDW-) LUDWIG INST CANCER RES.
Chen Y, Gout I, Gure A, OHare M, Pfreundschuh M, Sahin U, Scanlan
New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop proc for the diagnosis, monitoring or treatment of cancers
                                                                                                           WPI; 99-132448/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renal cancer associated antigen precursor sequence. Cancer associated antigen; diagnosis; research; trobreast cancer; colon cancer; gastric cancer; renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9904265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y07061 standard; Protein;
Y07061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Au-Young J, Bandma
WPI; 99-070259/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lal
                                                                                                                                                                 OHare M,
Scanlan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human DnaJ-like proteins - for cancer, immune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ָּט
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Pred.
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                                                                                                                                                              Obata Y, Old
MJ, Stockert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 257; DB 1;
No. 3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GDIFSHFFG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                              E E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment; humán;
nal cancer; lung c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for diagnosis,
                                 products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
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WESOLT WESOLT OF THE PROPERTY 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosts, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, remal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                         weight disorders, e.g. obesity, cachexia or anorexia nervosa, or a related disorder such as diabetes. The products can also be used to modulate cell cycle progression and apoptosis. They can be used for treating neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus Tub Interactor (mTI-3) protein.
serine protease; tub interactor; treatment; obesity; cachexia;
anorexia nervosa; diabetes; cell cycle progression; apoptosis;
neurodegenerative disease; Alzheimer's disease; drug screening;
parkinson's disease; Huntington's chorea; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 28; Fig 4; 120pp; English.
The sequence is that encoding the Tub Interactor protein (mTI-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM Errada PR, Gimeno CJ; WPI; 98-217246/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 456-457; 787pp; English.

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V11858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W59132
                                                                                                                                                         which are
                                                                                                                                                                                                                                                                                                                                                  related
                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1998.
05-SEP-1997; U15627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
WO9812302-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amylotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W59132;
                                   which are characterised by apoptosis, including Alzheimer's disease, Parkinson's disease, Huntington's chorea, amylotrophic lateral sclerosis or spinocerebellar degenerations. The products can also be used for detection, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1997; US-897340.
17-SEP-1996; US-715032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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                                                                                                                                                                                                                                                                                                                                   ich is a putative serine protease. TI genes function biochemical pathways involved in weight control and lated disorders. The products can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obesity, cachexia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 YEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKRDI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactor genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDKYGKEGL-NGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDPFEDFF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDILGVPAGASENELKKAYRKLAKEYHPDKNPQMQ----ETNFKEISFAYEVLSNPEKREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNQSRSRNGRRRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sclerosis; spinocerebellar degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - used to develop products for the treatment anorexia nervosa or related disorders e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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Pred. No. 2.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                     identify agents associated with induction of anergy

bisclosure; Fig 2; 3lpp; English.

The sequence represents a mouse cysteine string protein encoded by

a gene isolated from mouse T-cell clones 11.3.7 and 12.2 by a new

procedure for identification of genes associated with anergy. The

protein is expressed in resting T-cells but not in anergic T-cells.

To isolate proteins of this type, differential display is first

performed by generating cDNA from polyA+ mRNA with an oligo-dT

primer with 2 variable anchor nucleotides at the 3'-end, e.g.

Tl1786, using reverse-transcriptase. The resulting cDNA

populations are amplified by the polymerase chain reaction,

populations are amplified by the polymerase chain reaction,

common 4-5 nucleotide sequence combinations, e.g. Tl1785. After

gel electrophoresis of the products, bands unique to anergised or

non-anergised cells are excised, eluted, amplified, cloned and

createned Genes and proteins (and corresponding antibodies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse cysteine string protein: anergy; T-lymphocyte; differential display; cDNA; reverse transcription; pr
                                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD Bloom D, Fathman G; WPI; 96-068884/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
 effectiveness, and in drug Sequence 223 AA;
                                                             sequenced.
                                                                                                                                                                                                                                                                                                                    Identifying genes associated with T-cell anergy, and the proteins encoded by them - useful to elucidate the anergic state, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase chain reaction; cloning; gel electrophoresis;
antibody; diagnostic; immunoassay; autoimmune disease;
Sequence
                               autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T11788
                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1995;
23-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organ transplantation; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R90680 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 DYYKILGVDKNASEDEIKKAYRKRALMHHPDRHSGASAEVQKEEEKKFKEVGEAFTILSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKKKTRYDSGQDLDEEGMNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKRDIYDK---YGKEGLNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYYEVLGVQRHASPEDIKKAYRKLALKWHPDK----NPENKEEAERKFKQVAEAYEVLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ASGPGNFYFQF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDPFEDFFGNRRGPRGSRSRGTGSFFSAF 144
                               from this procedure may be used e.g. in monitoring une disease, organ transplantation, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438
                                                              Genes and proteins (and corresponding antibodies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    US-265100.
                                                                                                                                                                                                                                                                                                                                                                                                                                   U07958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.5%;
36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "In-frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "In-frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "In-frame stop codon"
                  screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DFDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                   JUNIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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Query Match Best Local Similarity

13.3%;

Score Pred.

227.5; DB 1 No. 1.6e-15;

DB 1;

Length

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1993; 143219.
25-OCT-1993; US-143219.
25-OCT-1993; US-953681.
29-SEP-1992; US-953681.
22-OCT-1993; US-141244.
(UYMC-) UNIV WCGILL.
(UNIW ) UNIV WASHINGTON.
Barber GH, Katze MG, KOrc
H. pylori GHPO 542 protein.
GHPO protein; Helicobacter
peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the bovine P58 protein, a cellular 58 kD protein purified from influenza-infected cells. The protein is used to reduce the accivity of a PKR protein (e.g. W36139) in a screening method for identifying anti-tumour agents by measuring PKR activity in a system before and after adding a test agent, where an increase in PKR activity indicates that the agent is an anti-tumour agent, especially useful for the prevention and/or treatment of neoplasms. PKR is an interferon-inducible cytoplasmic Ser-Thr specific protein kinase which can also be activated by double stranded RNA. PKR is active in cell growth and differentiation by regulating protein synthesis, and thus has been suggested to function as a tumour suppressor.
                                                                                                                    W98446 standard;
                                                                        31-MAR-1999
                                                                                                   W98446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening method for identifying increase in the activity of a dou
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N-PSDB; V01072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; PKR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W36140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taurus.
                                                                                                                                                                                                                                 MRKKFDD-GEDPLDAESQQGGGGNPFHRSWNSWQGFSPFSSGGPFR
                                                                                                                                                                                                                                                                            KRDIYDKYGKEGLNG---GGGGGSHFD-----SPFEFGFTFR 94
                                                                                                                                                                                                                                                                                                                          DYYKILGVKRNAKKQEIIKAYRKLALQWHPDNFQNEEEKKKAEKKFIDIAAAKEVLSDPE
                                                                                                                                                                                                                                                                                                                                                     DYYEVLGVQRHASPEDIKKAYRKLALKWHPD--KNPENKEEAERKFKQVAEAYEVLSDAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ne P50 protein.
n; PKR; double stranded RNA-activated growth; differentiation; tumour suppr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKRDI
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504 AA;
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                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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47.28;
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                                                                                                                 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504
                     infection;
                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          218.5; DB 1
No. 4.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy
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suppressor; tumourige
                     gastroduodenal
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d RNA-activated
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                   disease;
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Best Local
                                                                                                                         05-DEC-1997; U22104.
14-JUL-1997; US-891328.
05-DEC-1996; US-759625.
25-MAR-1997; US-823745.
(ASTR) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1998.

01-APR-1998; U06371.

29-JUL-1997; US-902615.

01-APR-1997; US-833457.

24-JUN-1997; US-881227.
                                               New
                                                                                  (ASTR ) ASTRA AB.
Alm RA, Castriotta LM,
WPI; 98-333051/29.
                                                                                                                                                                                                                                                                                           secreted protein;
                                                                   N-PSDB;
                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                            08-JUN-1999
                                                                                                                                                                                                                                                      WO9824475-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections and gastrointestinal diseases Claim 8; Page 773-774; 2054pp; English.
This sequence represents a Helicobacter pylori GHPO invention. The polypeptides can be used for preventinelicobacter infections, and gastroduodenal diseases the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                 Y11104 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               these infections, including acute, chronic, and atrophic peptic ulcer diseases, e.g. gastric and duodenal ulcers. used for the production of antibodies. The products can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INMR) MERIEUX ORAVAX PĀSTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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  pylori
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                       for
    and
Helicobacter pylori nucleic acids the diagnosis, prevention and tread other Helicobacter species
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Pred. No. 2.7e
84; Mismatches
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                                                                                                       Kabok
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No. 2.
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..7e-14;
                                                                                                       Smith
                     treatment
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Length 278;

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05-DEC-1997; U22104.
14-JUL-1997; US-891928.
05-DEC-1996; US-759625.
25-MAR-1997; US-823745.
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Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 97 ORFs are shown. The proteins are variously cell envelope proteins, cytoplasmic proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
97 ORFS are shown. The proteins are variously cell envelope proteins, cytoplasmic proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                       New isolated Helicobacter pylori nucleic acids - used to develop products for the diagnosis, prevention and treatment of infection by H. pylori and other Helicobacter species Claims 37, 41; Page 271-272; 339pp; English.

Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all,
                                                                                                                                                                                                                                                                                                                           (ASTR ) ASTRA AB.
Alm RA, Castriotta LM, Doig
WPI; 98-333051/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori. WO9824475-Al.
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H. pylori ORF hp7e10192_23712780_f2_5 cytoplasmi
Vaccine; probe; diagnostic; ORF; cell envelope proceed protein; cytoplasmic protein; cellular
                                                                                                                                                                                                                                                                                                             N-PSDB;
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Human; secreted protein; ATCC 98026;
cell proliferation; differentiation;
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Misc_difference

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14-APR-1997; U06139.
18-APR-1996; US-634325.
(GEMY) GENETICS INST INC.
JACODS K, LAVAILIE ER, MCCO
Spaulding V;
WPI; 97-526460/48.
N-PSDB; V02136.
New secreted proteins encoded clones present in ATCC 98026 -
possibly having cytokine, cell proliferation/differentiation
regulating, immunomodulating and many other activities
Claim 12; Page 78-79; 139pp; English.
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CC The present sequence represents a novel human secreted protein deposited CC under accession number AFCC 98026. The secreted protein can be used to CC determine biological activity, to raise antibodies, as tissue markers, CC to isolate cognate ligands or receptors, to identify agents that CC modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities although no evidence CC clal proliferation/differentiation modulating activity or induction of CC other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune CC diseases and allergy); regulation of hemanatopolesis (e.g. for treating canamia or as adjunct to chemotherapy); stimulation of growth of bone, CC cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, CC periodontal disease, neurological diseases stroke, fibrosis); inhibition CC contemplation of follicle stimulating hormone (for control of confections, tumours); haemostatic artivities (e.g. for treating contemplated; for treating septic shock, Crohn's disease); as a claiming contemplated is the use of the corresponding nucleic actid in gene contemplated is the use of the corresponding nucleic actid in gene
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Query Match Best Local S Matches 36 l Similarity 56.2 36; Conservative 10.3%; 10; Score 176; DB 1; Pred. No. 1.8e-10; 0; Mismatches 14 Length 159; Indels 4. Gaps 2

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Search completed: June 30, 2000, 09:57:24
Job time: 2725 sec

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Post-processing: Minimum Match 0%
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/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
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US-08-486-955A-6
US-08-974-546-2
US-08-872-534-4
US-08-872-534-4
US-08-813-219-26
US-08-8143-219-26
US-08-8143-219-26
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Query Match
Best Local Similarity
Matches 1330; Conserval
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                                                                                                                                                                                                                                                                                                                                                                 TYPE:
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Length 1330;

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Sequence 1, Appli	Sequence 1, Appli	Sequence 8, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 31, Appl	Sequence 31, Appl	Sequence 7, Appli	Sequence 1, Appli

ALIGNMENTS

Minimum DB Maximum DB

Sequence:

Run on:

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; LIBRARY: HNT2RAT01
; CLONE: 260873
US-08-868-288A-4
                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,288A
FILING DATE: June 3, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                         IMMEDIATE SOURCE:
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                                                                             STRANDEDNESS:
TOPOLOGY: lir
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CITY: Palo Alto
STATE: CA
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Query Match Best Local Sim Matches 1330;

Similarity

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Score 1307.2; Pred. No. 0; 0; Mismatches

В 0; 5

1330; 0;

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Gaps 60

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                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/868,28

APPLICATION NUMBER: 08/868,28

APPLICATION NUMBER: 3,197

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEPAX: 415-845-4166
                                                                                                                                    TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                            IMMEDIATE SOURCE:
LIBRARY: HNT2RAT01
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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                                                                                                                  SEQUENCE CHARACTERISTICS:
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CCITY: Palo Alto
STATE: CA.
COUNTRY: USA
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                                                           STRANDEDNESS:
TOPOLOGY: lin
                                                                                         TYPE: nucleic acid
                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGATTATGCGATCACGGATCAGTCAGAGCAGGGTCAGGAGACGGGGCTGACGGCACG
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Lal, Preet
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STRANDEDNESS: S:
TOPOLOGY: linear
TOPOLATE SOURCE:
LIBRARY: HNT2RA7;
CLONE: 260873
US-09-388-993-4
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                                           Query Match
Best Local Similarity
Matches 1330; Conserv
                                                                                                                                                                                                                                                                                                                                     STREET: 3174 POILET DRIVE

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,99
FILING DATE:
APPLICATION NUMBER: 08/868,288
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
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APPLICANT: AL YOUNG, Jan.
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO
                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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Matches 147; Conserv
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Sequence 2, Appr...
5922567
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ATTORIEY AGENT INFORMATION:
ATTORIEY BILLINGS, LUCY J.
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.855-0555
                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                        TOPOLOGY: line
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LENGTH: 1376 base pair
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: June 3, PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La1, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW
NUMBER OF SEQUENCES: 7
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CLONE: 136466
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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 GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAAGGCA 222
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                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                             1376 base pairs
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3174 Porter Drive
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                             Score 91.4; D
Pred. No. 5.5e
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                             DB 4;
5.5e-18;
hes 71;
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                                                       Length 1376;
                               Indels
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US-09-235-373-2
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                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/868,288 FILING DATE: June 3, 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
                                                                                                                           163 GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAGGCA 222
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283 GAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGG
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                                                                                                                                                                         Local Similarity
nes 147; Conserv
                                                                                                                                                                                                                                                                                                                                            LENGTH: 1376 base pairs
TYPE: nucleic acid
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CITY: Palo Alto
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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linear
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US-09-388-993-2
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Best Local Similarity
Matches 147; Conserv
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Patent No. 6
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AN-YOUNG, Janice
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preoti
APPLICANT: Bandman, Olya
TITLE OF INVENTION: TWO NEW HUMAN DNAJ-LIKE PROTEINS
NUMBER OF SEQUENCES: 7
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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APPLICATION NUMBER:
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CLONE: 136466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                         GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAGGCA 222
                   GACATCTATGACAAATATGGCCAAAGAAGGATTAAATGGTGG 383
                                                                  CAGGAGAAATTCCAGGATCTGGGTGCTGCTTATGAGGTTCTGTCAGATAGTGAGAAACGG
                                                                                     GAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGG
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Pred. No. 5.5e-18;
0; Mismatches 71;
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RESULT 8
US-08-974-546-2
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Best Local Similarity 58.5%;
Matches 148; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 672 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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REGISTRATION NUMBER: 20015
REGISTRATION NUMBER: A5:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/486,955A FILING DATE: 07-UN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FATHMAN, Garrison
APPLICANT: BLOOM, Debra
TITLE OF INVENTION: Anergy Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                      260 CGGAGCAGTTTGG 272
                                                                                                                                                           383 GNGGNGGNGGTGG 395
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                                                                                                                                                                                                                                                                                                                                                             203 CCGAGGATATTAAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                       143 CAATCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGGGGTGGAGAGACATGCCTCAC 202
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COUNTRY: US
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                         83 CAGATGACATTAAAAAGTCCTATCGGAAGCTGGCCCTGAAGTATCACCCTGACAAGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                 23 CACTOTOTACTTCCGGGGAATCGTTATACCATGTTCTTGGACTGGACAAGAATGCAACCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                               TGTCGGATGCTAAGAAACGGGACATCTATGACAAATATGGCAAAGAAGATTAAATGGTG
                                                                                                                                                                                          TGACAGACGCCACGAAAAGAAACATTTATGACAAGTATGGCTCGCTGGGGCTCTATGTGG
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Pred. No. 2.2e-13;
0; Mismatches 102;
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Sequence 4, Application US/08472534
Patent No. 5919620
GENERAL INFORMATION:
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELLEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, well C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
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LENGTH: 2349 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/9:
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                 343 GACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTGGNGGNGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                163 GATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAAGGCA 222
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                                                                                                                                                                                                                                                                                                                              171
                                                                                                                                                                                                                                                                                                                                                                223
                                                                                                                                                                                                                                                                                                                                                                                          111 GATTATTACAAGATTCTTGGGATCCCATCGGGGGCCAACGAGGATGAGATCAAGAAAGCC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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CLONE: 2525691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                             GGCCTGTATGACCAGTATGGGGAGGAAGGCCCTGAAGACCGGCGGTGG 331
                                                                                                                                                                                                                                                                      GAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGG 342
                                                                                                                                                                                                                                                                                                                     TACCGGAAGATGGCCTTGAAGTACCACCCAGACAAGAAT-----AAAGAACCCAACGCT 224
                                                                                                                                                                                                                                                                                                                                             TATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAAGAAGAAGCA 282
                                                                                                                                                                                                                                                    GAGGAGAAGTTTAAGGAGATTGCAGAGGCCTATGATGTGCTAAGTGACCCCCAAGAAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2349 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73.4; DB 4;
Pred. No. 2.2e-12;
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Matches
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TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Biov
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                 3328
                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_pept
3442 CAAAAACGTGCCTATGACCAGTATGGTGCTGCAGGCGCCAATGGTGGTTTTTGGTGGA 3501
                                                                  3385
                                                                                                                                                                                                  3268 AACAATACTGAATTTTATGATCGTCTGGGGGTATCCAAAAAACGCTTCGGCAGACGAAATC 3327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                  154 AACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATT 213
                                                                                                                                                                 214 AAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAAATCCTGAGAATAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- INFORMATION: /product= "NH2-terminal portion OTHER INFORMATION: DNA J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   Local Similarity
mes 146; Conserv
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                                                                                     GAAGAAGCAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCT 333
                                                                                                                                 AAAAAGGCTTATCGTAAGCTTTCCAAAAAATATCACCCAGATATCAACAAGGAGCCT---
                               AAGAAACGGGACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTGGNGGNGGNGGT 393
                                                               ---GGTGCTGAGGACAAGTACAAGGAAGTTCAAGAAGCCTATGAGACTTTGAGTGACGAC 3441
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New York
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1251 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of
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682..2502
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                                                                                                                                                                                                                                                                                   56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Heat-Shock Protein 72"
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Pred. No. 1.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                     1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20JUN1996
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                       1128 AAGAGGAAAGATTACTACAAGATTCTAGGAGTGGACAAGAATGCCTCTGAGGACGAGATC 1187
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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   322
                                                                                                                                                                                        154 AACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATT 213
                                                                                                                                      214 AAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 GGAAGTCATTTTGACAGT 411
                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C
                                                                                                                                                                                                                                          Local Similarity
mes 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0609.4260001/JAG/SRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 19JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                    AAGAAAGCTTATCGGAAACGGGCCTTGATGCACCATCCAGATCGGCATAGTGGAGCCAGT 1247
CTGTCGGATGCTAAGAAACGGGACATCTATGACA 355
                                 GCTGAGGTTCAGAAGGAGGAGGAGAAGAAGTTCAAGGAAGTTGGAGAGGCCTTTACTATC 1307
                                                                -CTGAGAATAAAGAAGAAGCAGAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1756 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gusella, James F.
VENTION: TPR-Containing Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                          Score 66.4; DB 4;
Pred. No. 2.4e-10;
D; Mismatches 71;
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N.W., Suite 600
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                                                                                                                                                                                                                                                                        Length 1756;
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RESULT 12
US-08-143-219-26
; Sequence 26, Application US/08143219
; Patent No. 5670330
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; MOLECULE TYPE:
US-08-221-8168-1
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TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1515 base pairs
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US-08-221-816B-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 124;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Katze, Michaell, Gary
APPLICANT: Witherell, Gary
APPLICANT: Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
TITLE OF INVENTION: OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                     1227
                                                                                                                                                                                                                                                                                                                                 1167 GTCACAGAGACGAGATTATTACAAAATCTTGGGAGTAAAAAGAAATGCCAAAAAGCAAGA 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/221. FILING DATE: 01-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COTUZZÍ, LEURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 79!
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                         324
                                                                                                                                                                                                                                                                                    210 TATTAAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAA-----AATCC 263
                                                                                                                                                                                                                                                                                                                                                            150 GTAAAACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGA 209
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                   CTCCGATCCAGAAATGAGGAAGAAGTTTGA 1376
                                                                                                                                                       GTCGGATGCTAAGAAACGGGACATCTATGA 353
                                                                                                                                                                                     AGAAGAAAAGAAAAAGCTGAGAAGAAGTTCATTGACATAGCAGCTGCTAAAGAAGTCCT 1346
                                                                                                                                                                                                              TGAGAATAAAGAAGAAGCAGAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCT 323
                                                                                                                                                                                                                                                             AATCATTAAAGCATACCGAAAATTAGCACTGCAGTGGCACCCAGACAACTTCCAGAACGA 1286
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No. 5738985
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Pred. No. 1.9e-08;
0; Mismatches 80;
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Best Local Similarity
Matches 124; Conserv
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MOLECULE TYPE: CDNA to
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1687 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
1462 CTCCGATCCAGAAATGAGGAAGAAGTTTGA 1491
                                                                          1402
                                                                                                                                       1342 AATCATTAAAGCATACCGAAAATTAGCACTGCAGTGGCACCCAGACAACTTCCAGAACGA 1401
                                                                                                                                                                                                              1282 GTCACAGAGACGAGATTATTACAAAATCTTGGGAGTAAAAAGAAATGCCAAAAAGCAAGA 1341
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: described
PRIOR APPLICATION NUMBER: 08/141,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 22,798
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPONOME. 707.
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OPERATING SYSTEM: PC-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,219
FILING DATE: October 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                      324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: September 29, 1992 ATTORNEY/AGENT INFORMATION:
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                                                                                                             264
                                                                                                                                                           210 TATTAAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAA-----AATCC 263
                                                                                                                                                                                                                                  150 GTAAAACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Douglas E. Olson REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 0 FILING DATE: October
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CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                 GTCGGATGCTAAGAAACGGGACATCTATGA 353
                                                                                            TGAGAATAAAGAAGAAGCAGAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCT 323
                                                                    AGAAGAAAAGAAAAAAGCTGAGAAGAAGTTCATTGACATAGCAGCTGCTAAAGAAGTCCT 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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611 West Sixth Street
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Katze, Michael G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA to mRNA
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Pred. No.
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                                                                                                                                                                                                                                                                                                                       Query Match
4.2%; Score 55.8; DB 1;
Best Local Similarity 3.5%; Pred. No. 9.5e-07;
Matches 9; Conservative 162; Mismatches 87;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                             1387
1207
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                381
                                                                                                                                                             261
                                                                                                                                                                                                                        201 ACCCGAGGATATTAAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAA 260
                                                                                                                                                                                                                                                                                         141 AACAATCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
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                              TGGNGGNGGNGGTGGAAG 398
                                                                                                                                            RRRRRRRRRRRRRRRR 1190
                                                                                           GCTGTCGGATGCTAAGAAACGGGACATCTATGACAAATATGGCAAAGAAGGATTAAATGG 380
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1800 Diagonal Road, Suite 500
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                                                                                                                                                                                                                                                                                                                                                      Length 7218;
                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 15 US-08-686-417-2 ; Sequence 2, Application U\$/08686417 ; Patent No. 5850018

GENERAL INFORMATION:

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Best Local Similarity
Matches 124; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/715,032
FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: S11Ver1, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-005CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,340
                                                                    1103
1163 CTCTCTGATCCCAAGAAAAAGACTCGTTATGACA 1196
                                                                                                                                      1043
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PRIOR APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD,
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                              322 CTGTCGGATGCTAAGAAACGGGACATCTATGACA 355
                                                                                                                                                           983 AAGAGGAAAGATTACTACAAGATCCTGGGAGTGGACAAGAATGCCTCTGAGGACGAGGATC 1042
                                                                                                                                                                                                                              154 AACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGAGACATGCCTCACCCGAGGATATT 213
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                  GCCGAAGTTCAGAAGGAGGAGAAGAAGTTTAAGGAAGTGGGAGAGGCCTTTACCATC 1162
                                                                                                  AAGAAAGCTTACCGGAAACGGGCCTTGATGCACCATCCAGATCGGCACAGTGGGGCCAGT 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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Pred. No. 5.9e-07;
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; NAME/KEY: COCATION: LOCATION: LOCATION: COCATION: US-08-686-417-2
Search completed: June 30, 2000, 13:33:04 Job time: 5945 sec
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NAME: MUTASHIQE, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 27112-20038.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-1500
TELEFAX: (202) 822-0168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 87
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ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,417
FILING DATE: 26-JUL-1996
CLASSIFICATION: 800
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baszczynski, Chris
APPLICANT: Barbour, Eric
APPLICANT: Horowitz, Jeannine
APPLICANT: Rosichan, Jeffrey L.
TITLE OF INVENTION: GENERAL AND EFFECTIVE EXPRESSION OF GENES IN PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                             2238 ATCCATTTGACATCTTCTCATCATT 2262
                                                                                                                                                                                2178 ATGATCAGTATGGTGAAGATGCCCTTAAGGAAGGAATGGGCGGTGGAGGATCCCATGTTG 2237
                                                                                                                                                                                                             350 ATGACAAATATGGCAAAGGAATAAATGGTGGNGGNGGNGGNGGTGGAAGTCATTTTGACA 409
                                                                                                                                      410 GTCCATTTGAATTTGGCTTCACATT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3748 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                       1 Similarity 60.0%; pred. No. 2.2e-06; 87; Conservative 0; Mismatches 58; Indels
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join(813..962, 2120..2284, 2376..2519, 2605..2880,
2970..3167, 3250..3573)
                                                                                                                                                                                                                                                                                                                                            0;
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Minimum DB
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Copyright (c) 1993 - 2000 Compugen Ltd.
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PS Claim 6; Fig 1A-D; 73pp; English.

CC This DNA encodes a human DnaJ-like protein, HSPJ1. The invention provides CC two human DnaJ-like proteins which are heat shock proteins J1 and J2 CC (HSPJ1 and HSPJ2) and nucleic acid sequences encoding the proteins. Host CC cells containing a vector comprising the nucleic acids are used for the CC production of recombinant proteins. Recombinant HSPJ1 and HSPJ2 are used to raise Ab, therapeutically and to screen for specific binding agents. CC Antagonists are used to treat or prevent a wide variety of solid cancers, CC leukaemia and lymphoma; immune disorders (typical of many disclosed are acquired immune deficiency syndrome, allergy, asthma, Crohn's disease, CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, microbial CC and parasitic infections) and inflammation. Agonists may be used to treat cor prevent tissue damage, e.g. in cases of ankylosing spondylitis, heart CC or prevent tissue damage, e.g. in cases of ankylosing spondylitis, heart CC attack, ischaemia, UV exposure, insulin-dependent diabetes and for wound CC healing, and may be expressed from a vector containing the nucleic acids. Fragments of the nucleic acids are used as primers and probes for CC detecting and quantifying the HSPJ-encoding nucleic acid in usual hybridisation and/or amplification assays, therapeutically as antisense, CC triplex-forming or ribozyme molecules, and for chromosome mapping.

SQ Sequence 1376 BP; 387 A; 268 C; 397 G; 322 T;
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10-DEC-1998.
02-JUN-1998; U11182.
03-JUN-1997; US-868288.
(INCY-) INCTE PHARM INC.
AU-YOUNG J, Bandman O, Lal P
WPI; 99-070259/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DnaJ-like protein; heat shock protein; bnaJ-like protein; heat shock protein; hmune disorder; inflammation; tissue
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" protein; HSPJ1; HSPJ2; cancer.

"mage; diabetes; wound
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08-OCT-1998.
01-APR-1998; U06371.
29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHPO protein; Helicobacter peptic ulcer disease; ss. Helicobacter pylori
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X14194;
                                                                                                                                                                                                         This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for the production of antibodies.
                                                                                                                                                                                                                                                                                                         New isolated Helicobacter polynucleotides - used to develop
for the diagnosis, prevention and treatment of Helicobacter
infections and gastrointestinal diseases
Claim 1; Page 853-855; 2054pp; English
                                                                                                                                                                                                                                                                                                                                                                                 (HDWA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
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                                                      TGAGTTATTATGAAATTTTAGAAGTGGAAAAACACAGCAACCAAGAGACCATTAAAAAGT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                           Similarity
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PO 885 gene.
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             memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so continuous trial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock Syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating to compute the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC
BATASH SC, Choi GH, Dillon P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus contig SEQ ID #219.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 969-972; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) and proteins der stored on computer readable medium
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RESULT X13034/1 ID 3034/1 
                                             infection.

To claim: Page 632-634; 2084pp; English.

Can computer readable medium has been developed which has recorded on it can be uncleotide sequences isolated from the Enterococcus faecalis genome. Can computer readable medium has been developed which has recorded on it can identify represent these nucleotide sequences which are primary can identify fragments of the Enterococcus faecalis genome with can identify fragments of the Enterococcus faecalis genome with can identify fragments of the products can be used to detect the presence commercial importance. The products can be used to detect the presence can identify fragments in samples. They can also be used for can be used for diagnosing Enterococcal infection in an animal and monitoring can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or can can be used to can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or can convert content of the products and for identifying agents which can be used to compute the growth or pathogenicity of Enterococcus faecalis, or can be used to content related organism, in vivo or in vitro. In particular the products related organism in vivo or in vitro. In particular the confidence of the products and for identifying agents which can be used to confidence organism. In vivo or in vitro. In particular the products are considered by the Enterococcus faecalis nucleotide sequences are considered organism.
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W09850555-A2.

12-NOV-1998.

04-MAY-1998; U08985.

14-NOV-1997; US-066009.

06-MAY-1997; US-044031.

16-MAY-1997; US-046555.
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      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis genome contig SEQ ID NO:97.
Enterococcus faecalis; contig; detection; Enterococvaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   olated Enterococcus faecalis polynucleotides and polypeptides to develop products for the detection of Enterococcus and for vaccines for prevention or attenuation of Enterococcus
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Pred. No. 6.2e:
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Best Local :
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                                                                                                                                                                                                                                                                                   pKA1. Cloud ... was isolated.
                                                                                                                                                                                                                                                                                                          cDNA of human origin and proteins coded by it expressed by in vivo or in vitro translation us antisense DNA corresponding to the cDNA.

Claim 1; Page 44-47; 167pp; Japanese.

mRNA expressed in human fibrosarcoma cell line isolated and used to construct a cDNA library upakal. Clone HP00067 encoding DNA J-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1993; J01095.
04-AUG-1992; JP-208077.
04-AUG-1992; JP-327619.
13-NOV-1993; JP-061431.
26-FEB-1993; JP-061431.
(SAGA) SAGAMI CHEM RES CENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                     Iwahori A, Kato S, Kato WPI; 94-065688/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA J like protein. Human cDNA; library;
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                                                    ATTATATGACAAAGGAGGAGAACAGGCAATTAAAGAGGGTGGAGCAGGTGGCGGT
                                                                        CATCTATGACAAATATGGCAAAGAAGGATTAAATGGTGGNGGNGGNGGTGGAAGT
                                                                                                           GAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGGGA 344
                                                                                                                                          TCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAAGAAGAAGCAGA 284
                                                                                                                                                                                     TTACTACGATGTTTTGGGGGTCAAACCCAATGCTACTCAGGAAGAATTGAAAAAGGCTTA 77
                                                                                              ----AAGTTTAAACAGATTTCTCAAGCTTACGAAGTTCTCTCTGATGCAAAGAAAAGGGA
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23-JUN-1994; US-265100.
(STRD) UNIV LELAND STAN
Bloom D, Fathman G;
WPI; 96-068884/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              populations are amplified by the polymerase chain reaction, using the same oligo-dT primer and a 5'-primer which includes common 4-5 nucleotide sequence combinations, e.g. T11785. After gel electrophoresis of the products, bands unique to anergised on non-anergised cells are excised, eluted, amplified, cloned and sequenced. Genes and proteins (and corresponding antibodies) arising from this procedure may be used e.g. in monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence encodes a mouse cysteine string protein isolated from mouse T-cell clones 11.3.7 and 12.2 by a new procedure for identification of genes associated with anergy. The protein is expressed in resting T-cells but not in anergic T-cells. To isolate proteins of this type, differential display is first performed by generating cDNA from polyA+ mRNA with an oligo-dT primer with 2 variable anchor nucleotides at the 3'-end, e.g. T1786, using reverse transcriptase. The resulting cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      effectiveness,
Sequence 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying genes associated with T-cell anergy, and the proteins encoded by them - useful to elucidate the anergic state, and identify agents associated with induction of anergy Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        differential display; cDNA; reverse transcription; probe polymerase chain reaction; cloning; gel electrophoresis; antibody; diagnostic; immunoassay; autoimmune disease;
                07-APR-1996 (first entry)
Human cysteine string protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R90680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9600300-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organ transplantation; vaccine; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse;
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07-APR-1996
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                                                                                                                                                                                                                                             323
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                                                                                                                                                                                                                                                                                                                                                                                                                       143 CAATCTCGTAAAACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCAC
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                                                                                                                                                 CGGAGCAGTTTGG
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                                                                                                                                                                                                                                           TGTCGGATGCTAAGAAACGGGACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTG
                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cysteine string protein; anergy; T-lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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 string
                                                                 cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug screening.
171 A; 173 C;
                                                                 672
protein; anergy;
                                                                  ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75.6; DB 1; Pred. No. 5.3e-12;
                                                                                                                                                                                                                                                                           -CAAGTTTAAGGAGATTAACAACGCACACGCCATCT
                  gene
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T-lymphocyte;
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RESULT 9
X20248_03
Continuation (4 of 10)
WP Sequence split into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In Identifying genes associated with T-cell anergy, and the proteins of encoded by them - useful to elucidate the anergic state, and pridentify agents associated with induction of anergy it identify agents associated with induction of anergy it identify agents associated with anergy in T-cells. Genes with at least CC for which is associated with anergy in T-cells. Genes with at least CC electrophores for detection of the anergic state, and may be used as probes for detection of the anergic state, and may be considered by a new procedure. Differential display is first component of the anergic state, and may be inside the procedure of the anergic state, and may be considered by generating cona from polyath man with an oligo-draw considered by generating conditions of the polyath man with an oligo-draw considered by the polyath man with an oligo-draw considered by the polymerase chain reaction, considered to a component and a first procedure which includes common 4-5 nucleotide sequence combinations, e.g. Til785. After considered considered delectrophoresis of the products, bands unique to anergised or consumenced. Genes and proteins (and corresponding antibodies) arising from this procedure may be used e.g. in monitoring confections and corresponding antibodies) arising from this procedure may be used e.g. in monitoring confections and corresponding antibodies) arising from this procedure may be used e.g. in monitoring confections and corresponding antibodies) arising from this procedure may be used e.g. in monitoring confections and corresponding antibodies) arising from this procedure may be used e.g. in monitoring confections and corresponding antibodies) arising from this procedure may be used e.g. in monitoring confections and corresponding antibodies) arising from this procedure may be used e.g. in monitoring confections are and proteins.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            effectiveness, and in drug screening.
Sequence 672 BP; 171 A; 173 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bloom D, Fathman WPI; 96-068884/07.
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23-JUN-1994;
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Fragment N

x20248_00

x20248_01

x20248_03

x20248_03

x20248_04

x20248_05

x20248_06
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                                                                                                                                                                                                                                                                   CGGAGCAGTTTGG
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                                                                                                                                     Name
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58.5%;
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RESULT X07570 ID X07570 ID X07570 ID X07570 ID X07 AC X07570 ID X07 AC X07570 ID X0757
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                                                                               Query Match
Best Local Similarity
Matches 137; Conserv
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Best Local Similarity
Matches 137; Conser
                                                                                                                                                                                                                                 Disclosure; Pages 55-56; 76pp; English.

The sequence is that encoding a secreted protein from a human fetal kidney clone AM610. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding secreted human proteins - are from foetal kidney or adult retina cDNA libraries, used as, potential vaccines
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29-JUN-1998; U13530
30-JUN-1997; US-8850
                                 166
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P-PSDB; W95710.
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(GEMY) GENETICS INST INC.
Agostino MJ, Evans C, Jacobs K,
Merberg D, Racie LA, Treacy M;
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x07570;
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Homo sapiens fetal kidney clone AM610 secreted protein gene.
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X20248_08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; fetal kidney;
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                                                                                                   58.5%;
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Pred. No. 4.6e
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214

AAAAAGGCATATCGGAAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAA AACAATACTGAATTTTATGATCGTCTGGGGGTATCCAAAAACGCTTCGGCAGACGAAATC 3327

273

3328

밁 Qy

3268

154 AACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATT

Matches

Conservative

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Indels

6

Gaps

1.

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PT Streptococcal heat shock proteins and corresponding DNA sequences - PT used in the production of a vaccine to treating and preventing PT strain-specific Streptococcal infection PS Claim 28; Page 90.94; 156pp; English.

PT This nucleotide sequence, isolated from a Streptococcus pneumoniae CC HindIII-partially digested genomic DNA library contains 2 open reading CC frames. The first encodes the heat shock protein 72 (HSP72) and the CC responding to the sequence encoding the N-terminus of the DnaJ protein. CC The sequence was isolated using a fragment of the chimaeric gene (T73392) CC corresponding to the sequence encoding the C-terminal 169 amino acids of 64755 daltons (as compared to 72 kb by SDS-PAGE), with a pI of 4.35. CT he protein Mas 58% and 85% identity to the E. coli and Lactococcus CC lactis HSP72 proteins respectively. The HSP72 protein and its fragment, CC or antibodies specific to HSP72, are used in pharmaceutical compositions, CC pref. a vaccine, for treating or preventing infection by S. pneumoniae or related bacteria in humans, e.g. S.pyogenes or S. agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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               Query Match
Best Local Similarity
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T73388;
01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995; US-472534.
04-AUG-1995; US-001805.
(IAFB-) IAF BIOVAC INC.
Brodeur B, Hamel J, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; S. pyogenes; open reading frame; heat shock protein E. coli; Lactococcus lactis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W22357-22358
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-052328/05
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19-DEC-1996.
17-MAY-1996; CA0322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding HSP72 and N-terminus of DnaJ protein. Streptococcus pneumoniae; S. pyogenes; S. agalactiae; genome; HSP72; open reading frame; heat shock protein 72; DnaJ; DnaK; chimaeric; E. coli; Lactococcus lactis; antibody; vaccine; infection; human; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
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/product= heat :
3265 .4320
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Best Local Similarity
Matches 146; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEO ID NO: 1 to 391 V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide
   1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide sequences - useful in diag
pharmaceutical compositions and vaccines
pneumoniae
Claim 1; Page 1144-1149; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can used in a computer-based system for identifying fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 98-272225
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                                                                                                                                                                                                                                                                                                                                                                                                                    invention can be used in diagnosis kits and assays, compositions and vaccines for S. pneumoniae. Sequence 7174 BP; 1990 A; 1347 C; 1611 G
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31-OCT-1996; US-029960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae genome of commercial importance, or expression modulating
fragments of the S. pneumoniae genome. Products from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOWA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a computer readable medium which nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) re
                                                                                                                                                                AACATGGTGGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGAAGCAGAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCT 333
                                                  AAAAAGGCATATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAGTCATTTGACAGT 411
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   AAAAAGGCTTATCGTAAGCTTTCCAAAAAATATCACCCAGATATCAACAAGGAGCCT---
                                                                                                                        AACAATACTGAATTTTATGATCGTCTGGGGGTATCCAAAAAACGCTTCGGCAGACGAAATC 1080
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                                                                                                                                                                                                                                                          Conservative
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56.6%;
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; S. pneumoniae; genome;
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Pred.
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No. 2.4e-09;
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                                                                                                                                                                                                                                                                                                                      Length 7174;
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GCAAAATTCAGAGAGTTGCAGAAGCATATGAAACACTCTCAGATGCTAATAGACGAAAA

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                                                                                                                                                                                                                                                                                                                                                                                        PT New polynucleotides encoding human secreted proteins - derived from PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, PT ovary, pituitary, retina and colon cDNA libraries
PT ovary, pituitary, retina and colon colon
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Best Local S
Matches 133
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EST clone AM610.
Expressed sequence tag; (
Expressed sequence tag; (
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Agostino MJ, Jacobs K,
Racie LA, Spaulding V,
WPI; 99-070076/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1195
                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor; ligand; anti-inflammatory; tumour inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V86438
                                                                                                                                                                                                                                                                                                                                                                          therapy
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10-APR-1997;
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                                                                                                                                                                                     166 TACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAGGCATAT 225
AGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGGGAC
                                             CACAAGTTGGCCATGAAGTACCACCCTGACAAAAAT - - - - - AAGAGCCCAGATGCTGAA
                                                                                           CGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAAGAAGAAGCAGAG
                                                                                                                                         TACTATGATATCTTAGGTGTGCCAAAATCGGCATCAGAGCGCCAAATCAAGAAGGCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                    331 BP;
                                                                                                                                                                                                                                     Conservative
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Pred. No. 8
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1.9e-10;
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encoded protein shows 29.45 percentage		E.I.	/*cdg= 11 /label= MG024	E) 13
		E F	.284	FT
	cds	FT	ty to fructos	T T
<pre>identity to spermidine/putrescine transport system permease protein (potB) from E. coli"</pre>		FT FT	<pre>/note= "Previously identified as MORF-20092, the encoded protein shows 45.96 percentage</pre>	H H
encoded protein shows 26.51 percentage		FT	- мG023	FT
/label= MG043 /note= "Breviously identified as MORE-20110.		17 F 17	73	F.T.
/*tag= q	CUS	H H	from E. col:	H F
		F I	protein shows 32.23 percentage	FT
putrescine transport ATP-binding protein		FT -	<pre>/note= "Previously identified as MORF-20084, the</pre>	H.
led protein shows 41.9		n in	/*tag= f	1 F
<pre>"Previously identified as MORF"</pre>		FT	cds 1747419243	
/*tag= p /label= MG042		17 1-13 18 18 18 18 18 18 18 18 18 18 18 18 18 1	<pre>percentage identity to 5,10-methylene-tetra- hydrofolate dehydrogenase (folD) from E. coli*</pre>	H) 17
5006051520	cds	FT	and MORE-20081, the encoded protein shows 33.04	Ŧ
phosphorialisterase (prsn) from Mycopiasika capricolum"		1. E. F.	<pre>/note= "Previously identified as MORF-19823, MORF-20080</pre>	H T
identity to phosphohistidinoprotein-hexose				9 19
/note= "The encoded protein shows 48.86 perc		FT	cds	
/abel= MG041		1 F. F.	modification protein (rimk) from Escherichia	Ψ Ψ
4937749643	cds	FT	the ribosomal protein	F
dehydrogenase (GUT2) from S. cerevisiae"		FT	d protein shows 31.50 percentage	H.
MORE-20106, the encoded protein snows 43.20		7 F	/notes "Draviously identified as MORF-20080 the	4 F
/note= "Previously identified as MORF-19831		FT	/*tag= d) F
Q		FT	cds complement (1357014247)	
complement (462684/422) /*tag= n	cas	Į,	Clostridium acetobutylicum"	13 H
146360 171331	2	F F		1 1
tity to glycerol kinase		FT	sly identifie	FT
<pre>_ reviously identified as MORE -20105, encoded protein shows 46.83 percentage</pre>		# F F	/label= MGO10	A.L.
/label= MG038		FT	cds 1206912725	
		FT	GB:D26185_102"	
complement (44751, .46277)	cds	HJ.	vered	¥1.
identity to histidyl-tRNA synthetase (hiss)		FT		1
encoded protein shows 30.71 percentage		FT		FT
<pre>/note= "Previously identified as MORF-20102.</pre>		E F	/label= MG009	H.
/*tag= 1		FI	cds 1125212040	
4054341787	cds	P.T.		
from B. subtilis"		T 1	encoded protein snows 2/.59 percentage	H H
encoded protein shows 48.13 percentage		FT		FT
<pre>/idder= mGU34 /note= "Previously identified as MORF-20101,</pre>		#J +	/label= MG006	E I
/*tag= k		FT	85529	
(91pr) from b. Subclifs (91pr) from b. Subclifs (3987340514)	cds	E 14	Key Location/Qualifiers	
identity to glycerol uptake facilitator		T FI	controlling method; open re	
encoded protein shows 35.90 percentage		FT.	M. genitalium; DNAA; DNA gyrase; origin of replication;	
<pre>/label= MG033 /note= "Previously identified as MORF-20100.</pre>		FT FT	27-MAR-1997 (first entry) Mycoplasma genitalium genome.	
/*tag= j	;	FT		
rrom B. Subtilis" 3924239904	cds	H 17	lard; DNA; 580073 BI	
identity to ATP-dependent nuclease (addA)		FT	400001	
encoded protein shows 26.82 percentage		FT.	300001	
/label= MG032		P F T	T58840_1 100001 210000 T58840_2 200001 310000	
/*tag= i	C	FT.	1	
from E. coli" 36987 38978	Cds	n ra	t into 6 fragments	WP Sec
percentage identity to GTP-binding protein		nj h	_0 _**	æι
/note= "Previously identified as MORF-19826		1 F		BESIII.

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                                                                                                                                                            Local
              TAAAGAAGAAGCAGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGA 329
                                                                                                                        GGATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAGGC 221
TCAAAAACAAAATGAGGAAAAGTTTAAAGAGGTTAATGAAGCATATGAAGTTCTAAGTGA
                                               TTTTAGAAAGCTTGCAATGCAATATCACCCCGATCGTCATAAAGCAGAAAATGAAACTAC
                                                                        ATATCGGAAACTGGCACTGAAGTGGCATCCAGATA------AAAATCCTGAGAA 269
                                                                                                GGATTATTATGAAGTTCTAGGGATATCTAAAAACGCTAGTTCTCAAGACATAAAAAAGAGC
                                                                                                                                                   142;
                                                                                                                                                             Similarity
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identity to deoxyribose-phosphate aldolase (deoC) from Mycoplasma pneumoniae" complement (64898. .65731)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system 54658.
                                                                                                                                                                                                                                                                                                                                                encoded protein shows 38.90 percentage identity to the protein disclosed in GB:D26185_104 from B. subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded protein shows 30.25 percer identity to the protein disclosed GB:D26185_99 from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= MG050
/note= "Previously identified as MORF-20117,
encoded protein shows 83.03 percentage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= MG049
/note= "Previously identified as MORF-20114
MORF-20115, the encoded protein shows 44.78
percentage identity to purine-nucleoside
phosphorylase (deoD) from E. coll*
59083. .59754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MORF-20114 and MORF-20115, the encoded protein shows 43.02 percentage identity to signal recognition particle protein (ffh) from B.
                                                                                                                                                                                                                                                                                                                                                                                                                       complement (65713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (56970.
                                                                                                                                                                                               encoded protein
                                                                                                                                                                                                                                                           (SPase)
                                                                                                                                                                                                                                                                        encoded protein shows 28.84 percentage identity to glutamic acid specific protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identity to sialoglycoprotease (gcp)
from Pasteurella haemolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded protein shows 36.60
                                                                                                                                                                                                           /label= MG070
/note= "Previously identified as MORF-20136,
                                                                                                                                                                                                                                                                                                 /note= "Previously identified as MORF-19845,
                                                                                                                                                                                                                                                                                                                                                                                      /note= "Previously identified as MORF-20123,
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= x
/label= MG057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Previously identified as MORF-20122,
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/label= MG056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Previously identified as MORF-19834,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= MG048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identity to spermidine/putrescine transport
                                                                                                                                                          5.0%;
                                                                                                                                                                                                                                                                                                                                      .82597
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                                                                                                                                                                                                                                                                                                               MG067
                                                                                                                                                Score 66; DB Pred. No. 4.300; Mismatches
                                                                                                                                                                                                                                                             Staphylococcus
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PT New isolated prostate-derived nucleic acids - used to develop PT products which may have cytokine, immune regulatory, haematopoiesis PT regulating, anti-inflammatory or tumour inhibition activity PS Claim 1; Page 455-456; 675pp; English.

CC X40438 to X40715 represent 5' expressed sequence tags (ESTs) for human CC secreted proteins expressed in prostate, and encode the proteins given in CC Y11716 to Y11993 respectively. The proteins given represent the signal CC peptide and an N-terminal fragment of a secreted protein. The nucleic CC acid sequences can be used for products for diagnosis and therapy. The CC They can also be used to develop products for diagnosis and therapy. The CC proteins obtained may have cytokine activity, cell proliferation and CC growth regulating activity, haematopoiesis regulating activity, tissue CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cc. receptor/ligand activity, anti-inflammatory activity, tumour inhibition contrivity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used cor obtaining corresponding promoter sequences. The nucleic acids cencoding the signal peptides can be used for directing extracellular consumptions are producted into a cell.

Sequence 336 BP; 92 A; 77 C; 105 G; 60 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST SEQ ID No: 291.
Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; Y11969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens. WO9906550-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X40691 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombolytic; anti-inflammatory; tumour inhibition; ds.
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Best Local
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                                                                                                                                                                           164 ATTACTATGAAGTTCTAGGCGTGCAGAGACATGCCTCACCCGAGGATATTAAAAAGGCAT
                                                                                                                                                   S
                                                                                                                                                                                                                      Local Similarity
ACATCTATGACAAATATGGCAAAGAAGGATTAAATGGTGGNGGNGGNGG
                                                                                                                       ATCGGAAACTGGCACTGAAGTGGCATCCAGATAAAAATCCTGAGAATAAAGAAGAAGCAG
                                                                  AGAGAAAATTCAAGCAAGTAGCGGAGGCATATGAAGTGCTGTCGGATGCTAAGAAACGGG
                                                                                             ATCGGAAGCTGGCGCTCAAGTACCACCCGGACAAGAACCCGGATGAGGGCGAG------
                                                                                                                                                   AGTACTATGACATCCTGGGCGTGAAGCCCAGCGCGTC-CCCGGAGAGATCAAGAAGGCCT
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                   4.9%;
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                                                                                                                                                                                                                  Score 65.6;
Pred. No. 2.
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                                                                                                                                                                                                                                   DB
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Db 220 ATGTTTATGACCAAGGCGGAGAGCAGGCAATBVAAGAAGGAGGCTCAGG 268

Search completed: June 30, 2000, 14:12:45 Job time: 8232 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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C.Species: Homo Sapiens (man) C.Species: Logary (man) R.Cheerham, M.E.; Brion, J.P.; Anderton, B.H. Blochem, J. 284, 463-76, 1992 R.Cheerham, M.E.; Brion, J.P.; Anderton, B.H. Richernce number: \$23508; MJID:92287055 A. Richernce number: \$23508; MJID:92287055 A. Reference number: \$23508; MJID:92287059 A. Refer	31 279 16.3 413 2 S35581 32 278 16.2 367 2 I40843 33 277 16.1 379 2 A47079 34 276.5 16.1 352 2 A39660 35 276 16.1 352 2 A39660 36 274.5 16.0 380 2 JC4739 37 274.5 16.0 419 2 T01643 38 273.5 15.9 369 2 B72327 40 271 15.8 369 2 T12472 41 270.5 15.8 376 1 HHECDJ 42 268.5 15.6 423 2 T09338 44 264.5 15.4 394 2 C64112 45 261.5 15.2 511 2 S38898 ALIGNMENTS
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RESULT 2
323508
dnaJ protein homolog - human
c, Species: Homo sapiens (man)
c, Species: Homo sapiens (man)
c, Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Dec-1999
c, Pacession: S23508

R; Cheetham, M.E.; Brion, J.P.; Anderton, B.H.

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Biochem. J. 284, 469
A;Title: Human homolo
A;Reference number: $
A;Accession: $23508
                                                                                                                                                                                                                                                                                                           heat-shock protein hsp40 - human
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994
C;Accession: JN0912; PN0688; PH0843
R;Ohtsuka, K.
Biophys. Res. Commun. 197, 235-240, 1993
A;Title: Cloning of a cDNA for heat-shock protein h
A;Reference number: JN0912; MUID:94071949
                                     A;Cross-references: GDB:3929189
A;Map position: 19pl3.2-19pl3.2
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal C;Keywords: heat shock; stress-induced protein C;Keywords: dnaJ amino-terminal homology <DNJ>
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A; Molecule type: mRNA
A; Residues: 1-351 <CHE>
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A; Residues: 1-340 <OHTl>
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8; MUID:92287055
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Pred. No. 7.8e
90; Mismatches
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7.8e-44;
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C;Superf
C;Keywor
RESULT 5
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heat shock protein homolog F2009.160 -
C;Species: Arabidopsis thaliana (mouse-
C;Date: 23-Apr-1999 #sequence_revision
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Query

Match

21

Score

364.5;

ВВ

'n

Length

340;

#sequence_revision 23-Apr-1999

#text_change thaliana

20-Sep-1999

Arabidopsis

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A; Nolecule type: DNA
A; Residues: 1-336 <BRID
A; Cross-references: EMBL: AF031926; N
A; Cross-references: EMBL: AF031926; N
                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T09133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bringaud, F.; Vedrenne, C.; Cu
Mol. Biochem. Parasitol. 94, 245
A;Title: Conserved organization
A;Reference number: 216580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Trypanosoma brucei
C; Date: 11-Jun-1999 #sequence
C; Accession: T09133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                   Superfamily: heat shock protein dnaJ; dnaJ; Keywords: heat shock; molecular chaperone;
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 32. Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shock protein homolog DNAJ -
ternate names: chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 NVNFGRS-----RSAQEPARKKQDPPVT-----HDLRVSLEEIYSGCTKKMKISHKRL
                                                                                                                                                                      SEDFFEDFFEDRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSS
                                                                         KKIYDSYGEEGLKGGVPDGSSGGPGGAGFHGFSSGGGTYNFSNRDAFKVFESFFGSNDPF
                                                                                                            RDIYDKYGKEGLNGG-----
                                                                                                                                                   IDYYKVLGVSRDASPSDIKKAYHQLALKYHPDKASGNREEAERLFKEVAEAYDVLSDEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPDGKSIRNEDKILTIEVKKGWKEGTKITFPKEGDQTSNNIPADIVFVLKDKPHNIFKRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPEDTFFGQRNGEEGM-----DIDDPFSGFP-----NGMGG---FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIYDKYGKEGL----NGGGGGGSHFDSPFEFGFTFR-NPDDVFREFFGGRDPFSFDFFE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GVADDDALXEERMRRG-----QNVLPAQPAGLRPPKPPRPASLLRHXPHCLSKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSFGGSGMGNFKSISTSTKMVNGRKITTKRIVENGQERVEVEE--DGQLKSLTIN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPFEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYYQTLGLARGASDEEIKRAYRRQALRYHPDKNKE--PGAEEKFKEIAEAYDVLSDPRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIFDRYGEEGLKGSGPSGGSGGGANGTS---
                                                                                                                                                                                                                            84;
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                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                            Conservative
DMFGG-
                                                                                                                                                                                                                                            21.2%;
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-GP---
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                                                                                                                                                                                                                        Score 363; DB Pred. No. 6.3e
                                                                                                              -GGGGSHFDSPFEFGFTFRNPD--DVFREFFGGRDPF 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.806; Mismatches
-GLHRVFRGFGGPHGFMSGFGS
                                                                                                                                                                                                                                                                                                                                                                                                              NID:g3452211; PID:g3452212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
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smatches 81;
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                                                                                                                                                                                                                                                                                                                   amino-terminal
stress-induced
                                                                                                                                                                                                                                          DB 2;
.3e-22;
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                                                                                                                                                                                                                                                             Length
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153
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protein
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                                                                         122
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RESULT 6
T30538
T30538
theat shock protein homolog dnaJ - Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF031927;
C;Genetics:
A:Gene: dnaJ
                                                                                                                                                                                                                                                                                                                                            R;Bringaud, F.; Vedrenne, C.; Cuvillier, A.; Parzy, D.; Baltz, Mol. Biochem. Parasitol. 94, 249-264, 1998
A;Title: Conserved organization of genes in trypanosomatids.
A;Reference number: Z16380
A;Accession: T30538
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A;Introns: 55/3; 204/2
A;Note: F2009.160
C;Superfamily: heat shock protein dnaJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T04618
R;Bevan, M.; Rose, M.; Hemp
submitted to the Protein Sa
A;Reference number: Z15380
A;Accession: T04618
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A; Residues: 1-338 <BRI>
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A; Residues: 1-348 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: AL021749
                                                                                                                                                                                             Query Match
Best Local
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                                                        VDYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKK 61
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   FAGG---
                                                                                                                     IDYYKVLGVGRNATPSDIKKAYHQLALKYHPDKCTGNREESERRFKEVSEAYDVLSDENK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTSFSSTSFGGSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDFFEDPFEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAVYDQYGEEGLKGNVPPPNAATSGASYFSTGDGSSSFRFNPRSADDIFAEFFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDYYKVLQVDRSANDDDLKKAYRKLAMKWHPDKNPNNKKDAEAKFKQISEAYDVLSDPQK 62
                             FSFDFFEDFFEDRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSS 156
                                                                                                                                                                                82;
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                                                                                                                                                                                              Similarity
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                                                                                                                                                                                Conservative
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                                                                                                                                                                                             Score 358; DB 2;
Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 361.5; DB 2
Pred. No. 8.7e-22;
                                                                                                                                                                                                                                                                                                                                 from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                    NID:g3452217; PID:g3452219; PIDN:AAC32777.1
   -GLHRVFRGFGGPQGFTSGFGS
                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                         Length 338;
                                                                                                                                                                                Indels
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                                                                                                                                                                               Gaps
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hypothetical protein F54D5 8 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T22648
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T22648
                                                                                                                                                                          submitted to the EMBL Data Library, A; Reference number: H00959 A; Accession: G02272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Coles, L.; Matthews, L.
submitted to the EMBL Data Library,
A;Reference number: Z19593
A;Accession: T22648
                                                                              F;4-68/Domain: dnaJ amino-terminal homology
                                                                                             A;Cross-references: EMBL:U40992; NID:g1127832; PIDN:AAC14483.1; PID:g1127833 C;Superfamily: dnaJ amino-terminal homology
                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-178 < WON>
                                                                                                                                                         A; Status: preliminary; translated from
                                                                                                                                                                                                                         R; Won, M.; Moon,
                                                                                                                                                                                                                                          C; Accession: G02272
                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997
                                                                                                                                                                                                                                                                                                           G02272
                                                                                                                                                                                                                                                                                                                        RESULT
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A; Introns: 46/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-331 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                        heat shock protein hsp40 homolog -
Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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nes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 DIYDKYGKEGL-----NGGGGGGGSHFDSPFEFGFTFR-NPDDVFREFFGGRDPFSFDF 114
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                                                                                                                                                                                                                                                                                                                                                                          HPKFKREG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        L----ED---KVLTVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVEVEEDGQLKSLTINGVADDDALXEERMRRGQNVLPAQPAGLRPPKPPRP-ASLLRHXP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEDPFEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTS 174
19.3%; ilarity 49.4%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289/2
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                                                                                                                                                                                                                                                                                                                                                                         244
                                                                                                                                                                                                                                                                                                                                                                                                        281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -AGGPGMF-----DLGGGAGGPNMFFMNQGGMDDG----
 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 343; DB
Pred. No. 2.5e
38; Mismatches
Score 332; DB 2;
Pred. No. 9.2e-20;
6; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                       -IKPGWKSGTKITFPKEGDQHPNRTPADIVFVIKDKP
                                                                                                                                                                                                                                                                                          human
                                                                                                                                                                                                            November 1995
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                                                                                                                                                             GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2,
2.5e-20;
75;
                                                                                 <DNJ>
 40;
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                                                                                                                                                                                                                                                         #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 331;
                              Length 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
 22;
Gaps
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DYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKR 62

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RESULT 10

F71623

protein with DnaJ domain PFB0090c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 26-Aug-1999
C;Accession: F71623
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; K
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.;
Science 282, 1126-1132, 1998
'.m(+)a. Chromosome 2 sequence of the human malaria parasite Plasmodium falc
       A;Title: Chromosome 2 sequence of the human malaria pare A;Reference number: A71600; MUID:99021743
A;Accession: F71623
A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal
F;2-67/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001307; GB:AE001273; NID:g3328757; A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of an obligate i A;Reference number: A71570; MUID:99000809 A;Accession: H71526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable heat shock protein J - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-C;Accession: H71526 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-392 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 107; Conserv
                                                                                                                                                                                                                                                                                218 CRGQGRIK-----DKRSVHVNIPAGVDSGMRLKMEGYGDAGQNGAPA
                                                                                                                                                                                                                                                                                                                                                         164
                                                                                                                                                                                                                                                                                                                                                                                           164
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                                                                                                                                                                                                                                                                                                                                                                                  FGSLGHGGLTSFSSTSFG-----GSGM-----GNFKSISTSTKMV-NGRKITTKRIV
                                                                                                                                                                                                                                                                                                                                                                                                                   FEGLFGGLGEAFGMRGGSESSRQGASKKVHITLSFEEAAKGVEKELLVSGYKSCD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDIYDKYGKEGLNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFD-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGQERVEVEEDGQLKSLTINGVADDDALXEERMR----RGQNVLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEDPF---EDFFGNRRGPRGSRSRG-----TGSFFSAFSGFPS--FGSGFSSFDTGFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESYDRYGKDGPFAGAGGFG-----GAGMGNMEDALRTFMGA---FGGDFGGNGGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGRRMG--GGRDSEEMEIDGDPFSAFGFSMNGYP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGNRRGPRGSRSRG----TGSFFSAF----SGFP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIYDQFGEEGLKGGAGGTDGQGGTFRYTF-HGDPHATFAAFFXGSNPFXI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIYDKYGKEGLNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDPFEDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ANTAKGVKVCDRCKGSGQVVQSRGFFSMASTCPDCSGEGRVITDPCSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 330; DB 2;
Pred. No. 3.4e-19;
7; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intracellular pathogen
                                                                        malaria parasite Plasmodium falciparum
                                                                                                          Cummings, L.M.; Aravind, L.; Koonin, G.G.; Clayton, R.; White, O.; Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                        translation
                                                                                                                                                                                                                                                                                                                   252
                                                                                                                                                                                                                                                                                   259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAC67936.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of humans: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-Oct-1999
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                        not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain UW3/Cx)
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S34630
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A; Cross-references: GB:
                                                                                                                                                                                                                            Query Match
Best Local
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Best Local S
Matches 85
                                                                                                                                                                                                                Matches
     112
                                       116
                                                                        63
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SVTLEDLYNGATRKLALQKNVICDKCEGRGGKKGAVECCPNCRGTGMQI--
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A;Cross-references: EMBL:L08069; NID:g306713; PIDN:AAC37517.1; A;Experimental source: umbilical vein endothelium R;Oh, S.; Twahori, A.; Kato, S. Biochim. Biophys. Acta 1174, 114-116, 1993 A;Title: Human cDNA encoding DnaJ protein homologue. A;Reference number: S34631; MUID:93326630 A;Accession: S34631
                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-273,'H',275-397 <IWA>
A;Residues: 1-273,'H',275-397 <IWA>
A;Cross-references: EMBL:D13388; NID:g219587; PIDN:BAA02656.1; PID:d1003160;
A;Experimental source: fibrosarcoma HT-1080
A;Experimental source: fibrosarcoma HT-1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Accession: S34630; S34631
R;Chellalah, A.; Davis, A.; Mohanakumar, T.
Biochim. Biophys. Acta 1174, 111-113, 1993
A:Title: Cloning of a unique human homologue
A;Reference number: S34630; MUID:93326629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dnaJ protein homolog - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-397 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: PFB0090c
C;Superfamily: heat shock protein dnaJ; dnaJ
F;21-89/Domain: dnaJ amino-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 FGGSGMGNFKSISTSTK---
                                                                                                                          Local Similarity
                                                                                  IYDKYGKEGLNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGG------RDPFSFDFF 115
      EDPFEDFFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSFSSTS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRDIYDKYGEEGLDKYGSNNGH-----SKGFKRTDPNDVFSKFFKTETKF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRDIYDKYGKEGLNGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDPFE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
85; Conserv
                                                                                                                                                                                                                                                                                                                      heat shock protein dnaJ; dnaJ amino-terminal homology dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                      Conservative
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ce: clone 3D7
                                                                                                                                                                                                                                          18.1%; 32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.1%;
                                                                                                                                                                                                                 30;
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                                                                                                                                                                                                             Score 311; Db 4, Pred. No. 1.2e-17; """ matches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AE001362; NID:g3845089; PID:g3845091; TIGR:PFB009
                                          -----FGSPMDIFDMFFGGGGRMQRERRGKNVVHQL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 327; DB 2;
Pred. No. 5.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----MVNGR----KITTKR
NRRGPRGS-----RSRGTGSFFSAFSGFPSFGS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID: 9306714
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                                                                                                                                                                                                                                                                                                                                                                                    PID:g219
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RESULT 13
G772128
heat shock protein J - Chlamydia pneumoniae (strain CWL029)
C;Species: Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: G72128
C;Accession: G72128
R;Kalman, S; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; C
Nature Genet. 21, 385-389, 1999
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis A;Reference number: A72000; MUID:99206606 A;Accession: G72128 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F39B2.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Introns: 50/3; 202/3; 350/1
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A;Cross-references: EMBL:Z92834; PIDN:CAB07390.1; GSPDB:GN00019; CESP:F39B2.10
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A;Reference number: 219498
A;Accession: T21991
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YYDVLGVKPDASDNELKKAYRKWALKFHPDKNPDGAEQ----FKQISQAYEVLSDEKKRQ 62
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A; Residues: 1-418 <BES>
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Best Local Similarity
Matches 98; Conserv
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A;Cross-references: EMBL:X77632; NID:g454913; PIDN:CAA54720.1; PID:g454303 C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology F;13-74/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S42031
R;Bessoule, J.J.; Testet, E.; Cassag submitted to the EMBL Data Library, A;Reference number: S42031
A;Accession: S42031
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001588; GB:AE001363; A;Experimental source: strain CWL029 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Allium porrum (leek)
C; Date: 06-Jan-1995 #sequence_revision
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C;Superfamily: heat shock
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-TKRIVENGQERVEVE---EDGQLKSLTINGVADD
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                                                                    NCASCQGSGMK - - - - -
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Pred. No. 4.6e-17;
97; Mismatches 98;
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A;Map position: 14L
G;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: heat shock; mitochondrion; stress-induced protein
F;6-70/Domain: dnaJ amino-terminal homology <DNJ>
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A;Molecule type; DNA
A;Residues: 1-409 <BEW>
A;Cross-references: EMBL:Z71340; NID:g1301940; PIDN:CAA95937.1; PID:e239683; PID:g130194
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A;Residues: 1-409 <BER>
A;Cross-references: EMBL:Ul2141; NID:g1314216; PIDN:AAA99647.1; PID:g994823
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
B;Bergez, P.; Dolgnon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
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A; Accession: S62992
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R;Atencio, D.P.; Yaffe, M.P.
Mol. Cell. Biol. 12, 283-291, 1992
A;Title: MASS, a yeast homolog of DnaJ involved in mitochondrial protein import.
A;Reference number: S26703; MUID:92107179
A;Accession: S26703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The sequence of a 44 420 bp fragment located on the left arm A;Reference number: S58711; MUID:96021608
A;Accession: S58714
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R;Bergez, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-409 <CA
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N;Alternate names: dhaJ protein homolog MAS5; protein N2418; protein YNL064c; protein
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Aug-1999
C;Accession: S26703; A39659; S58714; S62992; S17250
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J. Cell Biol. 114, 609-621, 1991
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A;Cross-references: GB:S74758; NID:g241522; PIDN:AAB20771.1; PID:g241523
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Best Local Similarity 29.7
Matches 95; Conservative
153 KGAVKKCTSCNGQGIKFVTRQMGPMIQRFQTECDVCHGTGDIIDPKDRCKSCNGKKVENE 212
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                                                                   173 TSF--SSTSFGGSGM---
                                                                                                                                                124 GNRRGPRG-SRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSL------GHGGL 172
                                                                                                                                                                                                                                                                               64 IYDKYGKEGLNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDPFEDFF 123
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                                                                                                             GGAQRPRGPQRGKDIKHEISA-----SLEELYKGRTAKLALNKQILCKECEGRGGK 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.4%; Score 298.5; DB 2; 29.7%; Pred. No. 1.2e-16; tive 36; Mismatches 86;
                                                                                                                                                                                                                                ----DDIFSQFFGA----
                                                           -GNFKSISTSTKMVNGRKITTK 206
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Search completed: June 30, 2000, 09:58:20 Job time: 940 sec

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Query Match

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15-FEB-2000 (Rel. 39, Last annotation update)
DNAJ PROTEIN HOMOLOG 2 (HEAT SHOCK J2 PROTEIN)
HSJ2 OR MRJ.
                                                                                                                                                                                                                       Chaperone.
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                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   Hunter P.J., Swanson B.J., Haendel M., Lyons G. Submitted (MAY-1998) to the EMBL/GenBank/DDBJ c-1- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Hunter P.J., Swanson B.J., Haendel M., Ly
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   FGGSGMGNFKSISTSTKMVNGRKITTKRIVENGQERVEVEEDGQLKSLTING
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PF00226; DnaJ; 1.
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217; Conserv
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93.5%;
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SCGGGAAGNYKSVSTSTEIINGKKITTKRIVENGQERVEVEEDGELKSLIING

(Rel. 22, Rel. 37, Rel. 39,

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FEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSFSST 178

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HSJ3_MOUSE
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15-FEB-2000 (Rel. 39,
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DNAJ PROTEIN HOMOLOG
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HSSP;
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berruti G., Perego L., Borgonovo B., Martega "MSJ-1, a new member of the DNAJ family of p cell-specific gene product."; Exp. Cell Res. 239:430-441(1998).
-!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-!- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
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Mus musculus (Mouse).
Mus musculus (Mouse).
                                                                                                                                                                                                                                   Chaperone.
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                                                               MVDYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAK 60
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KRDIYDKYGKEG-LNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFF-EDP 118
                                               MVDYYEVLGVPRQASAEAIRKAYRKLALKWHPDKNPEHKEEAERRFKQVAQAYEVLSDVR 60
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
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EMBL; X63368; CAA44969.1;
PIR; S23508; S23508.
HSSP; P25685; 1HDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"Human homologues of the bacterial heat-shock protein
preferentially expressed in neurons.";
Biochem. J. 284:469-476(1992).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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ALTERNATIVE PRODUCTS: TWO ISOFORMS; HSJIA AND HSJIB (
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: BRAIN (NEURONAL LAYERS). WEAKLY,
MUSCLE AND SPLEEN.
SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHOCK 40
                                                 DLALGLELSRREQ----
                                                                          DDALXEERMRRGQNVLPAQPA 255
                                                                                                                  SSTSFGGS-GMGNFKSISTSTKMVNGRKITTKRIVENGQERVEVEEDGQLKSLTINGVAD 234
                                                                                                                                                     LGPFSEL - - QNRG
                                                                                                                                                                             --PFEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSF
                                                                                                                                                                                                      KREIYDRYGREGLTGTGTGPSRAEAGSGGPGFTFTFRSPEEVFREFFGSGDPFA-ELFDD
                                                                                                                                                                                                                 KRDIYDKYGKEGLNGGGGGGSHFDSPF---EFGFTFRNPDDVFREFFGGRDPFSFDFFED
                                                                                                   SSSSFSFSPGAGAFRSVSTSTTFVQGRRITTRRIMENGQERVEVEEDGQLKSVTINGVPD
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00636; DNAJ_1;
PS50076; DNAJ_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92287055
                                                                                                                                                                                                                                                                                                                                                                                                         Neurone; Alternative splicing.
1 71 DNAJ-LIKE.
                                                                                                                                                                                                                                                                                                                                                                    275
278
351
                                                                                                                                                                                                                                                                                                       Conservative
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351 N
38783 MW;
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                                                 226
                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                   GGR -> DVF (IN ISOFORM HSJIA).
MISSING (IN ISOFORM HSJIA).
; 1FA290C6764665F3 CRC64;
                                                                                                                                                                                                                                                                                                                   Score 641.5;
Pred. No. 2.0
                                                                                                                                                                                                                                                                                                       ed. No. 2.6
Mismatches
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                                                                                                                                                                                                                                                                                                                   ,6e-42;
                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HSJ-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DnaJ
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                                                                                                                                                                                                                                                                                                                                351;
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                                                                                                                                                                                                                                                                                                       41;
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                                                                                                                                                     -SDF
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CONFLICT
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P25685;
                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92093635.
Raabe T., Manley J.
"A human homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HEAT SHOCK 40 KD PROTEIN 1 (HEAT SHOCK PROTEIN 40) (HSP40) (DNAJ
                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hata M., Okumura K., Seto M., Oht "Genomic cloning of a human heat and its chromosomal localization Genomics 38:446-449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human) 
Eukaryota; Metazoa;
 CONFLICT
                                            CONFLICT
                                                       CONFLICT
                                                                                                                       PFAM; PF00226; DnaJ; 1 PFAM; PF01556; DnaJ_C;
                                                                                                                                                                           EMBL; X62421; CAA44287.1; -.
EMBL; D49547; BAA08495.1; -.
EMBL; D85429; BAA12819.1; -.
EMBL; S20062; S20062.
                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                +
                                                                                                                                                                                                                                                                                                                                                             J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                           Qian Y.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 1-76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of a cDNA bacterial DnaJ.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohtsuka K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSPF1 OR DNAJ1 OR HDJ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN HOMOLOG
                                                                                                   DOMAIN
                                                                                                                                            PROSITE; PS00636; DNAJ_1; PROSITE; PS50076; DNAJ_2;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97131529
                                                                                                                                                                                                                                                                                                                                                                    (HDJ-1) J-domain."
                                                                                                                                                                                                                                                                                                                                                                                Nuclear magnetic resonance
                                                                                                                                                                                                                                                                                                                        MOI. BIO1. 260:224-235(1996).
SIMILARITY: INTERACTS WITH HSP70 AND CAN STIMULATE ACTIVITY. STIMULATES THE ASSOCIATION BETWEEN HSC70 SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
                                                                                                                                                                  1HDJ;
                                                                                                              shock;
                                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics
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 150
                                                                                                            Chaperone;
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81
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of the Escherichia
19:6645-6645(1991).
150
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136
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                                                                                                                                                                                                                                                                                                                                                                                            Hartl F.-U.,
                                                                                                            1.
3D-structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heat-shock protein hsp40, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-48
                                                                                                                                                                                                                                                                                                                                                                                 solution structure of
                                                                  REF.
                   SGGGANGTSFSYTFHGDPHAMFAEFFGGRNPFDTFFGQRNG
EEGMDIDDPFSGFPM -> TAEEPMVPLSATHSMETLMPCL
LSSSVAEIPLTPFLGSGTGRKAWTLMTHSLASLW (IN
                                                       G
                                                                            RGASDEEIKRAYRRQA
                                                                                        DNAJ-LIKE.
L -> Q (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 shock protein 40 to 19p13.2.";
                                                                                                                                                                                                                                                                                                                                                                                            McColl D.
(IN REF.
                                                        (IN REF. 1).
                                                                                        (IN REF.
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                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
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                                                                        . 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heat-shock protein.";
                                                                            AALGRGDQAGLPPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Hsp40)
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Best Local S
Matches 99
                                                                                                                                                                     EMBL;
HSSP;
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
                                                            PFAM; PF00226; DnaJ; 1. PFAM; PF01556; DnaJ_C; 1.
                                                                             FLYBASE; FB9n0015657; DnaJ-1.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PFAM; PF00226; DnaJ; 1.
                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             Lee J.Y., Palter K.B.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- INDUCTION: BY HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNJ1_DROME
Q24133;
                            DOMAIN
                                           Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last seque
15-DEC-1998 (Rel. 37, Last anno
DNAJ PROTEIN HOMOLOG 1 (DROJ1).
DNAJ-1 OR DROJ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Lee J.Y., Palter K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROME
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                                                                                                                                                                   U34904; AAC23584.1;
P25685; 1HDJ.
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    334
                                           Heat shock
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  DNAJ-LIKE.
; 6056A235D6F2DC89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 364.5;
Pred. No. 4.
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RESULT 7
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Best Local S
Matches 99
                                                                EMBL; L08069;
PIR; S34631;
HSSP; P25685;
MIM; 602837;
PRINTS; PRO0625; DNAJPROTEIN.
PROSITE; PSO0636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS50076; DNAJ_2; 1.
PFAM; PF00226; DnaJ; 1.
                                                                                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                       EMBL; D13388; BAA02656.1;
EMBL; L08069; AAC37517.1;
PIR; S34631; S34631.
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collable tween the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1174:111-113(1993)
-!- SIMILARITY: CONTAINS A DNAJ-LIKE DOMA
MOTIFS FOUND IN DNAJ PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
DNAJ PROTEIN HOMOLOG 2 (HSJ-2).
HSJ2 OR DNAJ2 OR HDJ2.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 93326629.
                                                                                                                                                                                                                                                                                                                                                                   "Human cDNA encoding DnaJ protein homologue.";
Biochim. Biophys. Acta 1174:114-116(1993).
                                                                                                                                                                                                                                                                                                                                                                                 Oh S., Iwahori A., Kato
"Human cDNA encoding Dna
                                                                                                                                                                                                                                                                                        heat shock protein
                                                                                                                                                                                                                                                                                              Chellaiah A., Davis A., Moh
"Cloning of a unique human
heat shock protein.":
                                                                                                                                                                                                                                                                                                                   Chellaiah
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 93326630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; C
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i; Hominidae; Homo.
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Pred. No. 7
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Best Loc
Matches
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P54102;
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REPEAT
REPEAT
REPEAT
CONFLICT
SEQUENCE
                                                                                      Genomics [2]
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                                                                                                                                                                                 Royaux I., Minner F., Goffinet A.M., de "A DnaJ-like gene, Hsj2, maps to mouse c 24 cM from the centromere.";
                                                                                                                                                                                                                                                             Mus musculus (Mouse), and Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
DNAJ PROTEIN HOMOLOG 2 (HSJ-2).
                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                  MEDLINE; 99017984.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               HSJ2 OR DNAJ2 OR RDJ1.
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GLY-RICH.
CXXCXGXG MOTIF.
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Pred. No. 6.5e-17;
0; Mismatches 72;
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Best Local
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                                                                                                                                                                               P71443;
15-JUL-1998
15-FEB-2000
15-FEB-2000
                                                                                                                                                                                                                              _LEPIN
                   Gul B., Ye Submitted
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SEQUENCE
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REPEAT
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PRINTS; PR00625; DNAJPOTEIN.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS00637; DNAJ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                Ballard S.A., Go M., So "Molecular analysis of serovar Copenhageni."; Gene 216:21-29(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM;
                                                                                                     STRAIN-WIJNBERG / MEDLINE; 98382569
                                                                                                                                          Bacteria;
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                                     STRAIN-SEROTYPE POMONA;
                                               SEQUENCE OF 1-35 FROM
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                     DNAJ_LEPIN
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                                                                                                                                                    Leptospira interrogans.
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        nitted (SEP-1996) to FUNCTION: INTERACTS
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141 C
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44868 MW;
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the EMBL/GenBank/DDBJ databases.
WITH DNAK, TO DISASSEMBLE A PROTEIN
ORIGIN OF REPLICATION. STIMULATES,
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                                                                                                               COPENHAGENI;
                                                                                                                                           Leptospiraceae;
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Pred. No. 1.9e
32; Mismatches
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GLY-RICH.
CXXCXGXG MOTIF.
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No. 1.9e-16;
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                                                                                           Adler B.;
                                                                                   Leptospira interrogans
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                                                                                                                                           Leptospira
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Best Local
 SEQUENCE FROM N.A.

Bessoule J.J., Testet E., C

"Cloning of a new isoform o

epidermal cells.",

Plant Physiol. Blochem. 32:

-!- FUNCTION: HAVE A CONTIN
                                                                                                                                                                                                                             01-NOV-1995
01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                                                                                              DNJ2_ALLPO
P42824;
                                                                                                                       Allium porrum (Leek).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Alliaceae; Allium.
                                                                                                                                                                                               LDJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REPEAT
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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PS50076; DNAJ_2; 1.
PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                          (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 37, Last annotation updat)
N HOMOLOG 2.
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 A CONTINUOUS
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35.2%;
32:723-727(1994)
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of a DnaJ protein
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CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
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Pred. No. 2.1e-16;
1; Mismatches 70
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RESULT 11
MAS5_YEAST
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Best Local :
                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MITOCHONDRIAL PROTEIN IMPORT PROTEIN MASS (PR
MASS OR YDJ1 OR YNL064C OR N2418 OR YNL2418C.
                                                                                                                                                    MAS5_YEAST
P25491;
                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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SEQUENCE
SEQUENCE
                          Saccharomycetaceae;
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PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS50076; DNAJ_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                QQKKVLE-----VHVEKGMQNGQ--KITFPGEADE
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                                                                                                                                                                                                                                                                             -TKRIVENGQERVEVE---EDGQLKSLTINGVADD
                                                                                                                                                                                                                                                                                                           NCASCQGSGMK-----VSIRQLGPGMIQQMQHPCNECKGTGEMISDKDRCPQCKGEKVV
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                                                                                                                                                                                                                                                                                                                                                                      -FGGGGSSRGRRQRRGEDYVHPLKVSLEDLYNGTSKKLSLSRNVLCTKCKGKGSKSGASM 162
                                                                                                                                                                                                                                                                                                                                                                                                          FFGNRRGPRGSRSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                      REIYDQYGEEGLKEGMGGGGGVHDPF-----DIFQSFFGGGG---
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rone: Repeat; Prenylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00684;
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83
81
148
164
191
207
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                                                                                                                                                                    STANDARD;
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88
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                          Saccharomyces
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32.7%;
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Pred.
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CXXCXGXG
FARNESYL
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GLY-RICH.
CXXCXGXG
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CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
FARNESYL (BY SIMILARITY).
DCE2A4DF192329E6 CRC64;
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Caplan A.J., Tsai J., Casey P.J., Douglas M.G.;

"Farnesylation of YDJIp is required for function at elevated growth temperatures in Saccharomyces cerevisiae.";

J. Biol. Chem. 267:18890-18895(1992).

-i- FUNCTION: PROBABLY INVOLVED IN MITCOHONDRIAL PROTEIN IMPORT. IS ALSO REQUIRED FOR EFFICIENT TRANSLOCATION OF PRE-PRO-ALPHA-FACTOR.

-i- SUBCELLULAR LOCATION: CONCENTRATED IN A PERINUCLEAR RING AS WELL AS IN THE CYTOPLASM (ACCORDING TO REF. 2).

-i- INDUCTION: MAS5 IS A HEAT SHOCK GENE WHOSE EXPRESSION INCREASES MODERATELY AT ELEVATED TEMPERATURES.

-i- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR CXXCCGXG MOTHERS FOUND IN DNAJ PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergez P., Doignon F.,
Yeast 12:297-297(1996).
[5]
REPEAT
REPEAT
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LIPID
                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bergez P., Doignon F., Crouzet M.;
"The sequence of a 44 420 bp fragment located on chromosome XIV from Saccharomyces cerevisiae.";
Yeast 11:967-974(1995).
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                                                                       Repeat;
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J. Cell Biol.
                                                                                             Chaperone;
                                                                                                                                                                                                                                                                                                                                                    the
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"Characterization of YDJ1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Atencio D.P., Yaffe M.P.;
"MAS5, a yeast homolog of DnaJ involved
                                                          DOMAIN
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S26703; S26703.
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                                                                                                                                                                                           L0002503; YDJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell. Biol. 12:283-291(1992).
                                                                                           PF00226; DnaJ; 1.
PF00684; DnaJ_CXXCXGXG;
PF01556; DnaJ_C; 1.
rone; Heat shock; Transp
                                                                                                                                                                                                       P25685; 1HDJ
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73
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72
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                                                                                           Transport;
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DNAJ-LIKE.
GLY-RICH.
CXXCXGXG M
CXXCXGXG M
CXXCXGXG M
CXXCXGXG M
CXXCXGXG M
                                                                                             Protein transport;
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           MOTIF
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Best Local 99
Matches 99
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P78004;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       EMBL; AE000015; AAB95781.1; -.
HSSP; P25685; 1HDJ.
PROSITE; PS00036; DNAJ_1; 1.
PROSITE; PS00076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC 29342
MEDLINE; 97105885.
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Bacteria; Firmicutes; Bacillus/Clostridium
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Nucleic Acids
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                                                                                                                                                                                                   FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN COMPLEX AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY WITH GRPE, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).
SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND TO EUKARYOTIC
                                                                                                                                                                                        DNAJ-LIKE PROTEINS
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Last annotation update
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Pred. No. 6.1e-16;
6; Mismatches 86;
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Best Local S
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                                                                                                                                    STRAIN-168 / MB11;
STRAIN-168 / MB11;
MEDLINE; 92250426.
Wetzstein M., Voelker U., Dedio J.,
Schlesswohl M., Herget C., Hecker M.
"Cloning, sequencing, and molecular
Bacillus subtills.";
J. Bacteriol. 174:3300-3310(1992).
                                                                                                                                                                                                                                                                DNAJ_BACSU
P17631;
01-AUG-1990
01-MAY-1992
15-JUL-1998
SEQUENCE OF 257-372
STRAIN-168 / JH642;
                       Wetzstein M., Dedio F., Schumann W., "Complete nucleotide sequence of the B Nucleic Acids Res. 18:2172-2172(1990).
                                                  STRAIN=168 / MB11;
MEDLINE; 90245667.
                                                                                             STRAIN=168 / JH642;
Kobayashi Y., Mizuno
Sato T., Takeuchi M.;
                                                                                                               SEQUENCE FROM N.A.
STRAIN-168 / JH642
                                                                     SEQUENCE OF 1-24 FROM
                                                                                    Submitted (MAY-1996) to the
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            BACSU
                                                                                                                                                                                                                             Bacillus subtilis.
Bacteria; Firmicutes;
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SEQUENCE
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PF01556;
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(Rel. 22,
(Rel. 36,
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DnaJ_C; 1.
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t C., Hecker M., Schumar
and molecular analysis
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Last sequence
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CXXCXGXG MOTIF.
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DNAJ-LIKE.
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on update)
                                                                                                    Takemaru
                                Bacillus
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                                subtilis dnaK gene.
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EMBL; D84432; BAA12465.1; -.
EMBL; D84327; BAA12677.1; -.
EMBL; D83717; BAA12077.1; -.
EMBL; D83717; BAA12077.1; -.
EMBL; D89501; S09501
PIR; S09501; S09501
PIR; S09501; S27506
PIR; S17506; S27506
PIR; B41874; B41874
HSSP; P08622; 1XBL
SUBTILIST; BG10665; DNAJTEIN.
PROSITE; PS00636; DNAJT; 1.
PROSITE; PS00636; DNAJT; 1.
PROSITE; PS00637; DNAJCXXXXXXG; 1
PROSITE; PS00637; DNAJCXXXXXXG; 1
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between
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"The dnak operon of Bacillus subtilis is heptacistronic.";
J. Bacteriol. 179:1153-1164(1997).
-i- FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN COMPLEX AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY WITH GRPE, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).
-i- INDUCTION: BY HEAT SHOCK.
-i- SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND TO EUKARYOTIC DNAJ-LIKE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                        EVE----EDGQLKSLT----
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PF00684;
PF01556;
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76 103 GLY-RICH.
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(62 169 CXXCXGXG MOT
188 195 CXXCXGXG MOT
192 209 CXXCXGXG MOT
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DnaJ_C; 1.
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01-FEB-1994
01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Plant dnaj homologue: molecular cloning, bacterial expres expression analysis in tissues of cucumber seedlings.";
Arch. Biochem. Biophys, 305:30-37(1993).

-I FUNCTION: HAVE A CONTINUOUS ROLE IN PLANT DEVELOPMENT IN THE STRUCTURAL ORGANIZATION OF COMPARTMENTS.

-I TISSUE SPECIFICITY: EXPRESSED IN SEEDLINGS IN ALL TISS EXCEEDINGLY HIGH LEVELS IN HYPOCOTYLEDONS AND ROOTS.
-I INDUCTION: WEAK, BY HEAT SHOCK.

-I SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN AND THE FOUR C MOTIFS FOUND IN DNAJ PROTEINS.
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
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PFAM; PF00584; DnaJ_CXXCXGXG;
PFAM; PF01556; DnaJ_C; 1.
Chaperone; Heat shock; Repeat.
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PROSITE; PSO0636; DNAJ_1; 1.
PROSITE; PSO0637; DNAJ_CXXCXG
PROSITE; PS50076; DNAJ_2; 1.
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Marberhaus F., Giebeler K., Bahl H.;

Marberhaus F., Giebeler K., Bahl H.;

"Molecular characterization of the dnak gene region of Clostridium acetobutylicum, including grpE, dnaJ, and a new heat shock gene.";

J. Bacteriol. 174:3290-3299(1992).

J. Bacteriol. 174:3290-3299(1992).

AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY OF DNAK (BY SIMILARITY).
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PROSITE; PS50076; DNAJ_2; 1.

PROSITE; PS00637; DNAJ_CXXCXGXG;

PFAM; PF00226; DnaJ_CXCXGXG;

PFAM; PF00684; DnaJ_CXCXGXG; 1.

PFAM; PF01556; DnaJ_C; 1.
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EMBL; M74569; AAA23247.1;
PIR; A41873; A41873.
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PRINTS; PR00625; DNAJPROTEIN.
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"Cloning, nucleotide sequence and structural
Clostridium acetobutylicum dnaJ gene.";
FEMS Microbiol. Lett. 114:53-60(1993).
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SIMILARITY: TO OTHER PROKARYOTIC DNAJ,
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O35723 mus musculu
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O49457 arabidopsis
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DnaJ.";
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ZHANG W., WAN T., YUAN Z., CAO X.;
"HSJ2, a novel human homologue of the
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"A new member of human dnaj-related gene family.";
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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61 KRDIYDKYGKEGLNGGGGGGSHFDSPFEFGFTFRNPDDVFREFFGGRDPFSFDFFEDPFE 120
                                                                                                               -
                                                                                                       241 AA; 26900 MW; D2F7F6BF CRC32;
                                                                                                                                                                                                                                             71.7%; Score 1230; DB 4; ilarity 100.0%; Pred. No. 1.1e-93; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Best Local Similarity 93:
Matches 217; Conservative
TISSUE=TESTIS;
MEDLINE; 99115;
PEI L.;
                                                                        095806;
095806;
01-MAY-1999
01-MAY-1999
01-NOV-1999
DNAJ-LIKE 2
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054946;

01-JUN-1998 ('

01-AUG-1998 ('

01-NOV-1999 ('

MRJ.

MRJ.

MRJ.

MUS musculus

Eukaryota; Mes
                        SEQUENCE FROM N.A
                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                              STRAIN-129; TISSUE-TROPHOBLAST;
HUNTER P.J., SWANSON B.J., HAEN
Submitted (MAY-1998) to the EMB
EMBL; AF035962; AAC16759.1; -
                                          Eutheria;
                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                  HSJ2.
                                                                                                                                                                                                                                                                                                                               HSSP; P25685; 1HDJ.
PROSITE; PS00636; DNAJ_1; 1.
PFAM; PF00226; DnaJ; 1.
SEQUENCE 242 AA; 27012 MW
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          99115663
                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                             lus (Mouse).
; Metazoa; Chordata; Craniata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
                                                                        (TrEMBLrel.)
(TrEMBLrel.)
(TrEMBLrel.)
PROTEIN.
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                                                                                                                  PRELIMINARY;
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                                        Chordata; Craniata;
Catarrhini; Hominida
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e EMBL/GenBank/DDBJ
                                                                               Created)
Last sequence Last annotation
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Last sequence update)
Last annotation update)
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Pred. No. 8.2e-88;
5; Mismatches 9; Ir
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                                         Hominidae;
                                                                               sequence update) annotation updat
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                                                Vertebrata;
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                                         Homo
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databases.
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                                                Mammalia;
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Query Match
Best Local S
Matches 163
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BERRUTI G., PEREGO L., BORGONOVO B.

"MSJ-1, a new member of the DNAJ fa
cell-specific gene product.";

Exp. Cell Res. 239:430-441(1998).

EMBL; U95607; AAC13944.1; -.

HSSP; P25685; 1HDJ.
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01-JAN-1998 (TrEMBLrel. 05, 1
01-NOV-1999 (TrEMBLrel. 12, 1
TESTIS SPECIFIC DNAJ-HOMOLOG
HSJ3.
                                                                                                                                                                                                                                    MGD; MGI:1306822; Hsj3.
PROSITE; PS00636; DNAJ_1;
PFAM; PF00226; DnaJ; 1.
SEQUENCE 242 AA; 26678
                                                                                                                                                                                                                                                                                                                                                                                                                            HSJ3.
Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 98189155.
                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Pituitary tumor-transforming gene protein associates with ribosomal protein S10 and a novel human homologue of DnaJ in testicular cells. J. Biol. Chem. 274:3151-3158(1999).

EMBL; AF080569; AAD16010.1; -.

HSSP; P5685; 1HDJ.

PROSITE; P590636; DNAJ 1; 1.

SEQUENCE 215 AA; 24051 MW; 49385BFB CRC32;
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Local Similarity
hes 197; Conserv
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             FEDFFGNRRGPRGSRSRGTGSFFSAFSGFPSFGSGFSSFDTGFTSFGSLGHGGLTSFSST 178
LENFFGDRRSTRGSRSRGAVPFSTSFTEFPGFGGGFASLDTGFTSFGSPGNSGLSSF-
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70.08;
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l; Mismatches
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Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata;
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                                                                                                                                                                                                                                      D3DCA2B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                 B., MARTEGANI E.;
family of proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                      Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
                                                                                                                                                                .8e-62;
les 37;
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3.7e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
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Best Local S
Matches 84
                                                                                                                                                                                                                                                                                                                        049457 PRELIMINARY;
049457 O49457
01-JUN-1998 (TrEMBLrel. 0)
01-JUN-1998 (TREMBLrel. 0)
01-NOV-1999 (TREMBLrel. 1)
HEAT-SHOCK PROTEIN.
F2109.160.
                                                                                                     SEQUENCE FROM N.A.
BEVAN M., KOETTER P., I
MEWES H.W., MAYER K., S
Submitted (FEB-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            076224
076224;
01-NOV-1998
01-NOV-1998
01-NOV-1999
CHAPERONE.
                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98418771.

BRINGAUD F., VEDRENNE C., CUVILLIER A., PARZY D., BALT BRINGAUD F., VENEGAS J., MERLIN G., BALTZ T.;

"Conserved organization of genes in trypanosomatids.";

MOI. Biochem. Parasitol. 94:249-264(1998).

EMBL; AF031926; AAC32771.1; -.

HSSP; P25685; 1HDJ.
  SEQUENCE FROM N.A.
EU ARABIDOES SEQUENCING PR
Submitted (APR-1998) to the
EMBL; AL021749; CAA16887.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00636; DNAJ_1; 1.
PFAM; PF00226; DNAJ_; 1.
PFAM; PF01556; DNAJ_C; 1.
SEQUENCE 336 AA; 36435 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma
                                                                                                                                                                                                                    Arabidopsis
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MEDLINE; 9841
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Similarity 50.6%;
84; Conservative 1
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                                                                                                     HEMPEL S., ENTIAN K.-D., SCHUELLER C.; to the EMBL/GenBank/DDBJ
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Pred. No. 2.7e-22;
l; Mismatches 45
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"Conserved organization of genes in trypanosomatids.";
MO1. Biochem. Parasitol. 94:249-264(1998).
BERBL; AF031927; AAC32777.1; -.
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                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00226; DnaJ; 1.
PFAM; PF01556; DnaJ_C;
SEQUENCE 338 AA; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
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PROSITE; PS00636; DNAJ_1;
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82; Conservative
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AA; 36535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinetoplastida;
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Pred. No. 3.7e
L9; Mismatches
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Pred. No. 6.9e-22;
0; Mismatches 39;
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                                                                                                                                                                                                                                                                                              Length 338;
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F54D5.8 PROTEIN.
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Q20774;
01-NOV-1996
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C
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HSSP; P25685; 1HDJ.
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
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                                                                                                                                                                                                     HCLSKEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKR
                                                                                                                                                                         HPKFKREG
                                                                                                                                                                                                                                                                                                                                                                                                                   FSSTSFGGSGMGNFK------SIS-----TSTKMVNGRKITTKRIVENGQE
                                                                                                                                                                                                                                                                                                                    RVEVEEDGQLKSLTINGVADDDALXEERMRRGQNVLPAQPAGLRPPKPPRP-ASLLRHXP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIYDQFGEEGLKEGGPGAGGGGGGMHYE-----FRGDPMNIFSSFFGGSDPFG---
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(OCT-1995) t
  (TrEMBLrel.
                                                   PRELIMINARY;
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                                                                                                                                                                                                                          281
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AA; 36265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AGGPGMF------DLGGGAGGPNMFFMNQGGMDDG----
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Last sequence update)
Last annotation update)
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Pred. No. 1.1e-20;
8; Mismatches 75;
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                                                   PRT;
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Best Local
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           EMBL; AF(
HSSP; P2:
PROSITE;
                                                                                                                                                                   075953;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
HEAT SHOCK PROTEIN HSP40-3.
                                                      TISSUE-COLON;
CHEN M.S., LASZLO A., ROTI ROTI J.L.;
"Differential response of members in
stress agents in mammalian cells.";
                                  Submitted (SEP-1998) to the EMBL; AF088982; AAC35860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) HEAT SHOCK PROTEIN HSP40-3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                   Eutheria;
                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                  075953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN M.S., LASZLO A., ROTI ROTI J.L.; "Differential response of members in the stress agents in mammalian cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P25685; 1HDJ.
PROSITE; PS00636; DNAJ_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 DYYEVLGVQRHASPEDIKKAYRKLALKWHPDKNPENKEEAERKFKQVAEAYEVLSDAKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 DYYKILGIPSGANEDEIKKAYRKMALKYHPDKNKE--PNAEEKFKEIAEAYDVLSDPKKR
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                                                                                                                                                                                                                                                                                                                                          NPDGRTVRTEDKILHIVIKRGWKEGTKITFPKEGDATPDNIPADIVFVLKDKPHAHFRRD
                                                                                                                                                                                                                                                                                                                                                     ----NGVADDDALXEERMRRG-----QNVLPAQPAGLRPPKPPRPASLLRHXPHCLSKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLYDQYGEEGLKTGGGSSGGSGGS---
                         P25685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00226; DnaJ; 1.
PF01556; DnaJ_C; 1.
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AP092536; AAC64141.1; -.
AP088983; AAC35861.1; -.
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            PS00636;
                                                                                                                                  Primates;
                                                                                                                                              Metazoa;
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                                                                                                                                                                                                                                 PRELIMINARY;
                        1HDJ.
DnaJ;
          DNAJ_1; 1.
                                                                                                                                 Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.8%;
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                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                       Created)
                                                                                                                                                                                 Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 339; DB 11;
Pred. No. 2.6e-20;
                                                                                                                                                                                                                                 PRT;
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Mus.
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Best Local S
Matches 97
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EMBL; Y12080; CAA72798.1; -.
HSSP; P25685; IHDJ.
PROSITE; PS00636; DNAJ_1; 1.
PFAM; PF00226; DnAJ; 1.
SEQUENCE 330 AA; 34596 MW;
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013303;
01-JAN-1998
01-JAN-1998
01-NOV-1999
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; anamorphic Tremellales; Cryptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECHT V., LUBECK M., KINDL H.; "Heat shock transiently enhances ribosome-associated DnaJ protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-ATCC 20509; MEDLINE; 98220306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribosome-associated curvatum.";
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SEQUENCE
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                                                               DPFSFDFFEDPFEDFFGNRRGPRGSRSRGTGSFFSAF--SGFPSFGSGFSSFDTGFTSFG 165
                                                                                                                                      RKIYDQFGEEGLKGGMPAGGGGGGPGFSS---FGAGGAAPASPSTPTDPNDIFNAFF---
                                                                                                                                                                      RDIYDKYGKEGLN-----GGGGGGSHFDSPFEFG------FTFRNPDDVFREFFGGR 107
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Pred. No. 8.3e
32; Mismatches
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Pred. No. 3.8e-20;
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01-NOV-1998 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
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EMEL; U41290; AABC7346.1; -.
HSSP; P25685; HLDJ.
PROSITE; PS00636; DNAJ_1; 1.
PRAM; PF00226; DnaJ; 1.
                            STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S.,
MITCHELL W.P., OLINGER L.,
DAVIS R.W.;
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Q13431;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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         "Genome Sequence of an O
Chlamydia trachomatis.";
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Science 0:0-0(1998).
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l Similarity 49.4%;
76; Conservative 1
                                                                                      trachomatis.
Chlamydiales;
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                  Obligate Intracellular Pathogen
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Last sequence
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EMBL/GenBank/DDBJ
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Pred. No. 4.2e-20;
6; Mismatches 40
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annotation update)
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                                      FAN J.,
                                                                                       Chlamydia
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SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
KALL
                                                                                                                                                                                                                                                                                              MEDLINE; 99021743.

GARDURR M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND GARDURR M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND KOONIN E.V., SHALLOM S., MASON T., YU K., FUJII C., PEDERSON J. SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M., SALZBERG S., ZHOU L., SUTTON G.G., CLAYTON R., WHITE O., SMITH | FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1998) to the EMBL; AE001307; AAC67936.1; HSSEP; P08622; 1XBL. PROSITE; PS00636; DNAJ_1; 1.
                                                                                                                                                                  EMBL; AE001370; AAC
HSSP; P08622; 1XBL.
PROSITE; PS00636; I
                                                                                                                                                                                                                                Science 282:1126-1132(1998).
EMBL; AE001370; AAC71808.1;
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01-MAY-1999 (TREMBLRel. 10,
01-NOV-1999 (TREMBLRel. 12,
PROTEIN WITH DNAJ DOMAIN.
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PFAM; PF01556; DnaJ_C; 1.
PFAM; PF00684; DnaJ_CXXCXGXG;
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                                                                                                                                      SEQUENCE
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Pred. No. 1.7e-19;
7; Mismatches 89
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   327;
No. 2.
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      DB 5;
.6e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                      WHITE O., SMITH H.O
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RA MEDLINE, 94150718.

RA MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA MILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA HONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,

RA LIGHTNING J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA THIERRY-MIEG J., THOMAS K., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

TO CORDER TO THE TOWN THE
                                                                            Matches
                                                                                              Query Match
Best Local
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Rhabditina;
[1]
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01-JUN-1998
01-NOV-1999
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045502;
                                                                                                                                                                                        Chaperone;
                                                                                                                                                                                                          PFAM; PF00226; DnaJ; 1.
PFAM; PF00684; DnaJ_C; 1.
PFAM; PF01556; DnaJ_C; 1.
PRINTS; PR00625; DNAJPROTEIN.
                                                                                                                                                                                                                                                                                   PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
-!- SIMILARITY: TO OTHER PROKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                       elegans.
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                                                                                                                                                                                                                                                                                                                          Z92834; CAB07390.1; P25685; 1HDJ.
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                                                                                                                                                                       DNA replication.
402 AA; 44308 MW;
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                            Score 309; DB 5;
Pred. No. 9.1e-18;
8; Mismatches 64;
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253	242	195	211	136	179	95	124	63	64
253 FVRKGDNLI 261	RMRRGQNVL 250	195 KKCNGKKQVKEDEIIEVGITPGMKDGEKFVFEGKGDEVIGIEKPGDFVVVLDEVEHEK 252	DGQLKSLTINGVAD	136 CKGCKGLGGNEGSAKECSDCRGRGIKV-RVIRMGPMVQQMQSHCDSCNGEGSTFLEKDRC 194	E	95 GGGRGGRGERVK	RGTGSFFSAFSGPPSFGSGFSSFDTGFTSFGSLGHGGLT	63 IYDQGGEEALQGGGGGGGFHNPF	EFGFTFRNPD
		52	41	.94	211	.35	.78	95	.23

Search completed: June 30, 2000, 11:53:57 Job time: 7114 sec

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Result
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Perfect score:
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(without alignments)
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_virus:*
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sp_unclassified:*
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                O35824 rattus norv
O36825 dictyosteli
O462530 arabidopsis
O22663 arabidopsis
O22663 arabidopsis
O23673 arabidopsis
O43177 solanum tub
O9zwk3 salix gilgi
O65160 zea mays (m
O14711 homo sapien
O24074 medicago sa
O16303 caenorhabdi
O66921 aquifex aeo
O20774 caenorhabdi
O9zfc5 methylovoru
O26953 trypanosoma
O74752 schizosacch
O26953 trypanosoma
O74751 mus musculu
                                                                                                                                                                                                                                                                                                                                                                     060884 homo sapien
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sapien
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45	44	43	42	41	40	39	38	37	36 6	<u>3</u> 5	34	33	32	31	. 30	29	28	27	26	25	24	23	22	21
377.5	378.5	382	385	387.5	389.5	390	392.5	398.5	401	401.5	402.5	403	405.5	406	410	417.5	426.5	429	431.5	436.5	436.5	438.5	439	441
20.0	20.1	20.3	20.4	20.6	20.7	20.7	20.8	21.2	21.3	21.3	21.4	21.4	21.5	21.6	21.8	22.2	22.7	22.8	22.9	23.2	23.2	23.3	23.3	23.4
413	379	383	316	382	378	383	498	379	392	412	389	369	368	392	331	377	408	402	348	385	377	379	354	328
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ALIGNMENTS

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                                                          Query Match 29.7%;
Best Local Similarity 37.9%;
Matches 130; Conservative 5
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HSSF; P25685; 1HDJ 1; 1.
PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
PFAM; PF00226; DNAJ_CXXXGXG; 1.
PFAM; PF00684; DNAJ_CXXXGXG; 1.
PFAM; PF01556; DNAJ_C; 1.
PFAM; PF01556; DNAJPROTEIN.
Chaperone; DNA replication; Repeat.
SEQUENCE 412 AA; 45745 MW; F88F73
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060884;
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LORAIN S., BRENDEL C., SCAMPS C., LECLUSE Y., LIPINSKI P
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

LORAIN S., BRENDEL C., SCAMPS C., LECLUSE Y.,
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                19 AVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLS
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ANVADTKLYDILGVPPGASENELKKAYRKLAKEYHPDKNPN---AGDKFKEISFAYEVLS
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                                                          Score 559; DB
Pred. No. 5.7e
56; Mismatches
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                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 129; Conser
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035824;
01-JAN-1998 (TREMBLEL 05,
01-JAN-1998 (TREMBLEL 05,
01-NOV-1999 (TREMBLEL 12,
                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
ANDRES D.A., SHOA H., FINLIN B.S.;
AICH. BIOCHEM. BIOPHYS. 0:0-0(1997).
-1- SIMILARITY: TO OTHER PROKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                            Chaperone;
SEQUENCE
                                                                                                                                                                                                                                                                                             PFAM; PF00226; DnaJ; 1.
PFAM; PF00684; DnaJ_CXXCXGXG;
PFAM; PF01556; DnaJ_C; 1.
PRINTS; PR00625; DNAJPROTEIN.
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
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                             228
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                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                          PROTEINS.
L; U95727; AAB64094.1; -.
P; P25685; 1HDJ.
ADQAPGVEPGDIVLFVQEKEHEVFQRDGNDLHMTYKIGLVEALCGFQFTFKHLDARQIVV
                    GEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHI
                                             GRFQMTQEVV------CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGE
                                                                                        MHPLKVSLEDLYNGKTTKLQLSKNVLCSACSGQGGKSGAVQKCSACRGRGVRIMIRQLAP
                                                                                                       DSEKRKQYDTYGEEGLKDGHQSSHG--DIFSHFFGD--FGFMFGGTPRQQDRNIPRGSDI 134
                                                                                                                                                                                       AVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLS
                                                                                                                                  NPEKRELYDRYGEQGLREGSGGGGGMDDIFSHIFGGGLFGFM--GNQSRSRNGRRRGEDM
                                                                                                                                                                            ANVADTKLYDILGVPPGASENELKKAYRKLAKEYHPDKNPN---AGDKFKEISFAYEVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S--RDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMVQQMQSVCSDCNGEGEVINEKDRCKKCEGKKVIKEVKILEVHVDKGMKHGQRITFTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYPPGKVIEPGCVRVVRGEGMPQYRNPFEKGDLYIKFDVQFPE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQAPGVEPGDIVLLLQEKEHEVFQRDGNDLHMTYKIGLVEALCGFQFTFKHLDGRQIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHPLKVSLEDLYNGKTTKLQLSKNVLCSACSGQGGKSGAVQKCSACRGRGVRIMIRQLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSEKRKQYDTYGEEGLKDGHQSSHG--DIFSHFFGD--FGFMFGGTPRQQDRNIPRGSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVDLEVTLEEVYAGNEVEVVRNKPVARQA----PGK----RKCN-CR---QEMRTTQLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPEKRELYDRYGEQGLREGSGGGGMDDIFSHIFGGGLFGFM--GNQSRSRNGRRRGEDM
                                                                                                                                                                                                                                                                          DNA replication.
412 AA; 45765 MW;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                     29.4%; Score 553; DI
37.6%; Pred. No. 1.80
Live 56; Mismatches
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Last annotation update)
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ae; Murinae;
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RESULT
Q42530
ID Q4
AC Q4
AC Q4
DT 01
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Best Local Similarity
Matches 145; Conserv
Q42530
Q42530;
Q1-NOV-1996
Q1-NOV-1999
Q1-
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"Cloning and analysis of a DnaJ homologue reveals its dual
localisation in the cytoplasm and cortex of Dictyostelium
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF063011; AAC72887.1; ...
HSSP; P25685; 1HDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00636; DNAJ_1; 1. Heat shock.
SEQUENCE 411 AA; 45654 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                HOMOLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKE-QLTEEAREGIKQLL-KQGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIVPGDVIVVLVQKEHPVFQRDGDDLVMEHELTLLEALTGFTFYITHLDGRVITVKNPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLYKGKVQKLALQK--SSKCPDCAGKGSTSKDGVKKCDDCHGQGFKVIHRQIGPGMVQKL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ
                                                                                                                                                                                                                                                                                                                                                                       QK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSQCPSCKGEGNVIREKDRCPKCKGNKTIQEKKTLEVNIDKGMKHGQKIVFPEEGDYESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDTYGEEGLKDGHQS-SHGDIFSHFFGDFGFWFGGTPRQQDRNIPR-GSDIIVDLEVTLE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISR--D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q-----EVV-----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGE-PHV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVYAGNFVEVVRNKPVARQAP------GKRKC-NCRQE---MRTTQLGPGRFQMT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDKYGEEGLKEGGAGFSPDDIFSLFFGGGG---FGGFGGRRGPRKGEPLQHNLKVTLE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYDILGVARDASETDIKKAYRKLAIKYHPDKNP-DPAAVEKFKELTVAYEVLSDTEKREL
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                                                     Created)
Last sequence update)
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Last sequence up
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Pred. No. 2.1e-37;
5; Mismatches 120;
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Best Local
ZHOU R., KROCZYNSKA B., MIERNYK J.A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ-1- SIMILARITY: TO OTHER PROKARYOTIC DNAT PROTEINS.
                                                                                                                                              022663;
01-JAN-1998
01-JAN-1998
01-NOV-1999
ATJ3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                       IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00226; DnaJ; 1.
PFAM; PF00684; DnaJ_C; 1.
PFAM; PF01556; DnaJ_C; 1.
PRINTS; PR00625; DNAJPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MENDEL; 6785; Arath;1253;6785.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS00636; DNAJ_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZHOU R., KROCZYNSKA B., I
Submitted (MAR-1995) to
-I- SIMILARITY: TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                          022663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ
                                                                                                                                                                                                                                                                  VVKPDSYKAISDEGMPIYQRPFMKGKLYIHFTVEFP-DSLSPDQTKALEAVLPKPSTAQL
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P25685; 1HDJ.
L; 6785; Arath;1253;
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420 AA; 46444 N
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35.8%;
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the EMBL/GenBank/DDBJ
R PROKARYOTIC DNAJ, ANI
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                                                                                                                                                         , Created)
, Last sequence up
, Last annotation
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Pred. No. 2.6e-37;
1; Mismatches 118
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Best Local
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HSSP; P25685; 1HDJ.
MENDEL; 26451, Arath;1253,26451.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1
PROSITE; PS00636; DNAJ_1; 1.
PFAM; PF00226; DNAJ_1; 1.
PFAM; PF00286; DNAJ_CXCXGXG; 1.
PFAM; PF00584; DNAJ_CXCXGXG; 1.
PFAM; PF01556; DNAJ_CXCXGXG; 1.
PFAM; PF01655; DNAJPROTEIN.
Chaperone; DNA replication.
SEQUENCE 420 AA; 46444 MW; CO3
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Q43177;
                                                                                                        EMBL; X94301; CAA63965.1; -.
HSSP; P25685; 1HDJ.
MENDEL; 10642; Soltu;1253;10642.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PROSITE; PS00636; DNAJ_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                          NANA:
Solanum tuberosum (Potato).
Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
euphyllophytes; Spermatophyta; Magnollophyta; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                LEGGEWIE G., BRAUN H.P., SCHMITZ U.K
Submitted (DEC-1995) to the EMBL/Geni
-!- SIMILARITY: TO OTHER PROKARYOTIC
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
TISSUE=LEAF;
                                      PFAM; PF00226; DnaJ; 1.
PFAM; PF00684; DnaJ_CXXCXGXG;
PFAM; PF01556; DnaJ_C; 1.
                     PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDTYGEEGLKDGHQSSHG-----DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEV
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                   PR00625;
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                   DNAJPROTEIN
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Pred. No. 2.6e-37;
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Q9ZWK3;
Q9ZWK3;
01-MAY-1999 (TIEMBLIFEL: 10, C
01-MAY-1999 (TIEMBLIFEL: 10, L
01-NOV-1999 (TIEMBLIFEL: 12, L
                                                                                                                                                                                                              "Expression of general and Dnak in the content of the EMBL/GenBank/DDBJ databases. Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     Chaperone;
SEQUENCE
                                                                                                                                                        MENDEL; 35038; Salg1;1253;35038.

PROSITE; PS00636; DNAJ_1; 1.

PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
                                                                                                                                                                                   EMBL; AB015601; BAA35121.1;
HSSP; P25685; 1HDJ.
MENDEL; 35038; Salg1;1253;39
                                                                                                                                                                                                                                                                               "Expression of genes
                                                                                                                                                                                                                                                                                                                                                       Salix gilgiana.
Eukaryota; Viridiplantae;
euphyllophytes; Spermatoph
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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mes 130; Conserv
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                                   FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ
                         YYEVLGVSKSASQDDLKKAYRKAAIKNHPDKGGD
 YDTYGEEGLKDGHQS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVTLEEVYAGNF--VEVVRN------KPVARQAPGKRKCN-CR-QEMRTT--QLGPGRFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDQYGEDALKEGMGGGGGGHDFFDIFSSFFGGSPFG---GGGGSSRGRRQRRGEDVVHPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDTYGEEGLKDGHQSSHG-----DIFSHFFG--DFGFMFGGTPRQQDRNIPRGSDIIVDL
                                                                                    Similarity
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                           ISHII-MINAMI N.,
                                                                                                                                    replication.
AA; 46563 M
                                                                                                                                                                                                                                                                                                                                            Rosidae;
                                                                                                                                                                                                                                                                                                                                       ilplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; eurosids I; Malpighiales; Salicaceae; Salix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ã,
                                                                                                                                   46563 MW;
                                                                                  27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.4%;
-SHG--DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLE
                                                                                                                                                                                                                                                                 I N., HAYASHIDA N., SHINOHARA K.; proteins homologous to the bacterial and DnaK in the Japanese willow (Sal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΜW,
                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                       Score 526; DB 10;
Pred. No. 2.9e-35;
5; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 534; DB 10; Pred. No. 6.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                    84A45244 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
                        ----PEKFKELAQAYEVLSDPEKREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112;
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                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 419;
                                                                       Indels
                                                                                                                                                                                                                                 EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                               420;
                                                                                                                                                                                                                                                                     (Salix
                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359
                                                                                                                                                                                                                                 DNAJ-LIKE
                                                                    Gaps
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                                               85
                        69
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065160
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                                                                                                                                                                                         Query Match
Best Local S
Matches 125
                                                                                                                                                                                                                                                                                  MENDEL; 29613; Zeama;1253;29613.
PROSITE; PS00637; DNAJ_CXXXXXXGXG; 1
PROSITE; PS00636; DNAJ_1; 1.
PEAM; PE00226; DnaJ, 1.
PEAM; PE00226; DnaJ, 2.
PEAM; PF00684; DNAJ_CXXXXXXGXG; 1.
PEAM; PF01556; DNAJ_C; 1.
PRINTS; PR00625; DNAJPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                065160;
                                                                                                                                                                                                                                                                                                                                                                                                          BASZCZYNSKI C.L.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND TO EUKAR
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF053468; AAC08009.1;
HSSP; P25685; 1HDJ.
MENDEL; 29613; Zeama;1253;2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
BASZCZYNSKI C.L., BARBOUR
Maydica 42:189-201(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays (Maize).
Eukaryota; Viridiplantae;
euphyllophytes; Spermatopi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrembLrel. 07, 01-AUG-1998 (TrembLrel. 07, 01-NOV-1999 (TrembLrel. 12, DAJ-RELATED PROTEIN ZMDJ1.
                                                                                                                                                                                                                                                                      Chaperone;
    186
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poaceae;
                                                        140
                                                                                  70
                                                                                                            98
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                                                                                                                                  14 YYEILGVPKSASQDDLKKAYRKAAIKNHPDKGGD----PEKFKELAQAYEVLSDPEKREI
                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
    OMTOEVVCDECPNV
                                                                                              YDTYGEEGLKD--GHQSSH---GDIFSHFFG-DFGFMFGGTPRQQDRNIPRGSDIIVDLE
                                                                                                                                                    FYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQ
                          VSLEDLYNGTSKKLSLSRNVICSKCKGKGSKSGASMRCPGCQGSGMKVTIR-
                                                   VTLEEVYAGNEVEVVRNKPV----
                                                                              YDQYGEDALKEGMGGGGSHVDPFDIFSSFFGPSFG---GGGGSSRGRRQRRGEDVVHPLK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLL-KQGSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVVKPDQFKAINDEGMPMYQRPFMRGKLYIHFSVEFP-DSLSPDMCKALEAVLPPRASVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTVTGDIVFVLQQKDHPKFKRKGDDLFVEHTLSLTEALCGFQFVLTHLDGRQLLIKSQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISRD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSFEDLYNGTSKKLSLSRNVICSKCKGKGSKSGASSKCAGCQGSGMKVSIRHLGPSMIQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQEVV-------CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTLEEVYAGNF--VEVVRN-----KPVARQAPGKRKC-NCR---QEMRTTQLGPGRFQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDQYGEDALKEGMGSGGSGAHDPFDIFQSFFGG-GNPFGGGGSSRGRRQRRGEDVIHPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQHACNECKGTGETINDKDRCPQCKGEKVVQEKKVLEVVVEKGMQNGQKVTFPGEADEAP
                                                                                                                                                                                        al Similarity 35.0
125; Conservative
                                                                                                                                                                                                                                                          DNA replication.
419 AA; 46725 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                      27.3%; Score 515; DB 10; 35.8%; Pred. No. 2.3e-34; tive 61; Mismatches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ε,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence up
Last annotation
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                                                   ----ARQAPGKRKCNCRQEMRTTQLGPGRF 185
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KLVNEERTLEVEIEPGVRDGMEYPFIGEGE
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                                                                                                                                                                                                                                                        CRC32;
                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                         115;
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H
                                                                                                                                                                                                                 Length 419;
                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWENSON
                            -QLGPSMI
                                                                                                                                                                                        48;
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                                                                                                                                                                                     Gaps
                          184
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229
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RESULT
O14711
ID O27
AC O2
D7 O D7 O
D7 O O2
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          014711;
014711;
01-JAN-1998
01-JAN-1998
01-NOV-1999
DNJ3/CPR3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00226; DnaJ; 1.
PFAM; PF00684; DnaJ_CxXCXGXG;
PFAM; PF01556; DnaJ_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00625; DNAJPROTEIN.
Chaperone; DNA replication.
SEQUENCE 415 AA; 46306 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF011793; AAB69313.1; -.
HSSP; P25685; 1HDJ.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYERS M., ELLEDGE S.J.; Submitted (JUL-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             117
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297
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                                                                                                       GEGEPHVDGEPGDLRFRIKVVKH-PIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHK
                                                                                                                                                                                                                  GPGRFQMTQEVV-----
                                                                                                                                                                                                                                                                                                     DIIVDLEVTLEEVYAGNFVEVVRNKPVARQA----PGK----RKCN-CR---QEMRTTQL
                                                                                                                                                                                                                                                                                                                                                                       ANVADTKLYDILGVPAGASENELKKAYRKLAKEYHPDKN---PQMQETNFKEISFAYEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQE-KFQDLGAAYEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPGEVVKPDQFKAINDEGMPIYQRPFMKGKLYIHFTVEFPDSLAPEQCK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D--KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAPDIVIGOIVFVLQQKDHSKFKRKGEDLFYEHTLSLTEALCGFQFVLTHLDNRQLLIKS
                                      VHIS--RDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPK
                                                                                                                                                                       APGMVQQMQSVCSDCNGEGEVINEKDRCKKCEGKKVIKEVKILEVHVDKGMKHGQRITFT
                                                                                                                                                                                                                                                          DMMHPLKVSLEDLYNGKTTKLQLSKNVLCSACSGQGGKSGAVQKCSACRGRGVRIMIRQL
                                                                                                                                                                                                                                                                                                                                                SNPEKRELYDRYGEQGLREGSGGGGWHGLIFSLTVFCGGLFGFM--GNQSRSRNGRRRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHYDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISR
IVVKYPPGKVIEPGCVRVVRGEGMPQYRNPFEKGGLYIKFDVQFPE
                                                                                 GEADQAPEWNPETLFFLLPGEKNMEVFQRDGNDLHMTYKIGLVEALCGFQFTLSHLDGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .C., LIEGEOIS ELLEDGE S.J.;
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8 (TrEMBLrel.
9 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.1%;
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12,
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                                                                                                                                                                                                -----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 509.5; DB 4;
Pred. No. 6.4e-34;
5; Mismatches 122;
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annotation update)
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                                                                                O24074 PRELIMINARY;
O24074;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
        Eukaryota; Virid euphyllophytes; core eudicots; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ZSZ6;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hevea brasiliensis (Para rubber tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ZSZ6
           Medicago sativa (Alfalfa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoide
                                                                       DNAJ-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaperone;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF085275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Physiol. 119:363-363(1999)
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Medicago
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PROSITE; PS00637; DNAJ_CXXCXGXG;
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MENDEL; 36329; Hevl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.H., YANG J., CHOW K.-S., HAN K.-H.;
evea brasiliensis homolog of DnaJ (HvDnaJ)
                                                                                                                                                                                                VKPDQFKAINDEGMPMYQRPFMRGKLYIHFSVDFPDSLPPDQCKALEAVLPSRTSVQ
                                                                                                                                                                                                              TRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQ
                                                                                                                                                                                                                                                              GEPGDLRFRIKVVKHPIFERRGDDLYTNVTVSLVESLVGFEMDITHLDGHKVHISR-DKI
                                                                                                                                                                                                                                                                                                QHPCNECKGTGETINDKDRCPQCKGEKVVQEKKVLEVIVEKGMQNGQRITFPGEADEAPD
                                                                                                                                                                                                                                                                                                                                                SLEDLYNGTSKKLSLSRNVICSKCKGKGSKSGASMKCSGCQGSGMKVSIRQLGPSMIQQM
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                                                                                                                                                                                                                                                                                                                                                                                                YDQYGEDALKEGMGSGGGAHDPFDIFQSFFGGNPFGGGGSSRGRRK---EGEDVIHPLKV
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                                                                                                                                                                                                                                                 TITGDIVFVLQQKEHPKFKRKGDDLIVDHTLSLTEALCASQFILTHLDGDLLIKSQPGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 35.9
28; Conservative
                                                                         PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA replication.
415 AA; 46072 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hevbr; 1253; 36329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD12055.1;
                                                                                                                                                                                                                                                                                                                       EVV-----CDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHVD
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05,
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Last sequence update)
Last annotation updat
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Pred. No. 8.5e
63; Mismatches
                                                                                   Created)
Last sequence update)
Last annotation updat
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AF085275) (F
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            Papilionoideae;
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(PGR99-
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Best Loc
Matches
  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
WILSON R., AINSCOUGH R., AINSCOUGH R., DONFIELD J., BURTON J., CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ000995; CAA04447.1; -.
EMBL; AF069507; AAC19391.1; -.
HSSP; P25685; 1HDJ.
MENUEL; 26909; Medsa;1253;26909,
PROSITE; PS00637; DNAJ_CXXCXGXG; 1
PROSITE; PS00636; DNAJ_1; 1.
PFAM; PF00226; DNAJ_1; 1.
PFAM; PF00184; DNAJ_C; 1.
PFAM; PF01556; DNAJ_C; 1.
PFAM; PF01556; DNAJ_C; 1.
PRAM; PF01556; DNAJ_C; 1.
PRAM; PF01556; DNAJ_C; 1.
                                                                                                    O16303
O16303;
O1-JAN-1998
O1-JAN-1998
O1-NOV-1999
TO5C3.5 PROT
                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
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STRAIN-CV. RANGELANDER;
FRUGIS G., MELE G., GIANNINO
Submitted (AUG-1997) to the
                                                                     Rhabditina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chaperone;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRUGIS G., MELE G., GIANNINO D., MARIOTTI D.;
"Isolation and characterization of a DnaJ-like gene from alfalfa.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND TO EUKARYOTIC DNAJ-LIKE
                                                                                                                                                                                                                               308
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                                                                                                                                                                                                                             GEVIKPGQHKAINDEGMPQHGRPFMKGRLYIKFSVDFP 345
                                                                                                                                                                                                                                                                                    QMQHVCPDCKGTGEVISERDRCPQCKGNKITQEKKVLEVHVEKGMQQGHKIVFEGQADEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFP 327
                                                                                                                                                                                                                                                                                                                                                              KVSLEDVYNGTTKKLSLSRNALCSKCKGKGSKSGTAGRCFGCQGTGMKITRRQIGLGMIQ
                                                                                                                                                                                                                                                                                                                                                                                    EVTLEEVYAGNEVEV-VRNKPVARQAPGK-----RKCNCR---QEMRTTQLGPGRFQ
                                                                                                                                                                                                                                                                                                                                                                                                          YDQYGEDALKEGMGGGAGSSFHNPFDIFESFFG-AGFGGGGPSRA--RRQKQGEDVVHSI
                                                                                                                                                                                                                                                                       PDTITGDIVFVLQVKGHPKFRRERDDLHIEHNLSLTDALCGFQFNVTHLDGRQLLVKSNP
                                                                                                                                                                                                                                                                                                                                             MTQEVV----
                                                                                                                                                                                                                                                                                                                                                                                                                                YDTYGEEGLKDGHQSSHG-----DIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121;
                                                                                                                  PROTEIN.
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21; Conservative
                                                                                                                          (TrEMBLrel.) (TrEMBLrel.)
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423 AA; 47197 MW;
                                                                    Rhabditoidea;
                                                                                                                                                                        PRELIMINARY;
                                                                                Nematoda;
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35.8%;
   CONNELL
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ANDERSON K., BAYNES C., BERKS CONNELL M., COPSEY T., COOPER
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                                                                    pda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                          Created)
Last sequence up
Last annotation
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Pred. No. 9.6e
57; Mismatches
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EMBL/GenBank/DDBJ databases
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066921 ID 0 AC 0 DT 0 DT 0

066921 066921; 01-AUG-1998 01-AUG-1998

PRELIMINARY; (TrEMBLrel. (TrEMBLrel.

07, 07,

Created)

sequence update)

PRT;

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Best Local
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF01556; DnaJ_C; 1.
PFAM; PF00684; DnaJ_CXXCXGXG;
PRINTS; PR00625; DNAJPROTEIN.
Chaperone; DNA replication.
SEQUENCE 439 AA; 47514 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF016428; AAB65361.1; --
HSSP; P25885; 1HDJ.
PROSITE; PS00637; DNAJ_CXXCXGXG;
PFAM; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
BLANCHARD M., BRADSHAW H., K
Submitted (AUG-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WATERSTON R.;
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STRAIN-BRISTOL N2;
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                                       366
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                                                                                                                                          --PRQQDRNIPRGSDIIVDLEVTLEEVYAGNEVEV-VRNKPVARQAPG------KRKCN 170
                                                                KEQLTEEAR
                                                                                                           LVGFEMDITHLDGHKVHIS--RDKITRPGAXXWKKGEGLPNFDNNNIKGSLIITFDVDFP 327
                                                                                                                                                                                                                                                                                                                          DTYGEEGLKDGHQSS-----HGDIFSHFFG-------DFGFMFGGT-----
                                                                                                                                                                                                                                                                                                                                                                              YKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
                                       KEHFLDDEK
                                                                                          LCGYNFLIKHLDGHPLVLSSKQGDVIKPGVIRGVLGKGMPNKKYPELKGNLFVEFEVEFP
                                                                                                                                                                                                  ACRGRGVKTIVQQIGPGMLQQMQ-VHCDACKGSGGKVPAGDKCKGCHGEKYENVSKILEV
                                                                                                                                                                                                                           -CR-QEMRT--TQLGPGRFQMTQEVVCDECP------NVKLVNEERTLEV
                                                                                                                                                                                                                                                     GGPRRR-----KFQDTVHPLNVTLEELYVGKTSKLKLSKKALCKTCEGSGGKKGEKYKCD
                                                                                                                                                                                                                                                                                                          DARGLEGVQGGGAGGGGGGFPGGLFSHFFGGAGGDDDDDDDDDDDMGGHPFGGLFGGMGGMGR 131
                                                                                                                                                                                                                                                                                                                                                             YTTLNVRPDASQADIKKSYFKLAKEYHPDKNPDH---GDKFKEISFAYEVLSSPEKRRLY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                        374
                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Score 495; DB 35.0%; Pred. No. 1.1e tive 56; Mismatches
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EMBL/GenBank/DDBJ
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.1e-32;
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Matches 128
 Q20774 PRELIMINARY;
Q20774;
Q20774;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-NOV-1999 (TrEMBLrel. 12, L
F54D5.8 PROTEIN.
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DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.N. "The complete genome of the hyperthermophilic bacaeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF01556; DnaJ_C; 1.
PFAM; PF00684; DnaJ_CXCXGXG;
PRINTS; PR00625; DNAJPROTEIN.
SEQUENCE 376 AA; 41963 MW;
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Bacteria; Aquificales;
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GKK-VEELLKQ
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                                                                                                                                                                                                 TLDGEKVKVKIPPGTKEGELIKVPGKGMPRLKGSG-RGDLYVRVHIDVPKIGVLSKLLGD
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                                                                                                                                                                                                                                                       --LVVEGKGHAGRYGGPPGDLYIIVKVKPHKIFERKGDDLYVDVNITYPEAVLGTEVEVP
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Pred. No. 2.2e-32;
1; Mismatches 118
                                                                       PRT;
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                sequence update) annotation updat
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01-NOV-1999 (T:
PUTATIVE DNAJ.
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COU
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULLON I.
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNST
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHA
PARSONS J., PERCY C., MCMURRAY A., MORTIMORE B., SUUNDERS D., SHOW
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans.";
Nature 368:32-38(1994).
EMBL; Z66513; CAA91334.1;
HSSP; P25685; 1HDJ.
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                                                                                                                                                                                                                                                                                EPGYRDGMEYPFIGEGEPHYDGEPGDLRFRIKVYKHPIFERRGDDLYTNYTYSLYESLYG
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                (TrEMBLrel. (TrEMBLrel.
                                          (TrEMBLrel.
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llarity 32.4%;
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                annotation
                              sequence
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Indels Length

91;

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120

113

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174 152

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O'CALLAGHAN JOHNSTON

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HSSP; P08622; 1XBL.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
Chaperone; DNA replication.
SEQUENCE 371 AA; 41052 MW; 1A24F423 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SSI, DSM11726;
EOM C.Y., KIM Y.M.;
"grpE, dnaK, and dnaJ genes of Methylovorus sp. strain SSI DSM11726.";
submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO OTHER PROKARYOTIC DNAJ, AND TO EUKARYOTIC DNAJ-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNAJ.
Methylovorus sp. strain SS1.
Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
Methylovorus.
[1]
                                                                                                                                                                                                                                                                                                                                            173 MQQGFFSVQQTCPKCHGSGKMVKEPCPSCQGAGRVKKHKTLSVKIPAGVDEGDRIRLSGE
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